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GenCore version 5.1.6
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                    Copyright
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8, 2005, 10:32:41 ; Search time 19.3721 Seconds (without alignments) 84.435 Million cell updates/sec Run on:

US-09-020-393B-3_COPY_42_58 96 1 FEHCNFNDVTTRLRENE 17 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched: of hits satisfying chosen parameters: Total number

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* PIR_79:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ð			SUMMARIES	
Result No.	Score	Query Match	* Query Match Length	DB		Description
-	96	100.0	128	<u>:</u>	RWHU59	surface glycoprote
7	63	65.6	126	~	136914	CD59 protein - bab
n	63	65.6	128	N	136894	protein -
4		48.4	1302	~	T20767	hetical pr
Ŋ	9	48.4	1767	~	T20766	hypothetical prote
ø	46	47.9	284	~	E83557	
7	46	47.9	777	7	E83748	hypothetical prote
æ	45	46.9			AB0022	probable membrane
σ	45	46.9			T21283	hypothetical prote
10	44	45.8	205		H71639	NADH2 dehydrogenas
11	44	45.8	807	7	D69102	collagenase - Meth
12	43	44.8	544		841626	spike protein chai
13	42	43.8	365	7	T20652	hypothetical prote
14	42	43.8	419	N	C83681	
15	42	43.8	434		AE1326	hypothetical prote
16	42	43.8	434		AG1697	
17	42	43.8	464	~	T16889	
18	41	42.7	117		69669	
19	41	42.7	179		S23358	•-
20	41	42.7	223		VCBVCA	coat protein - tob
21	41	42.7	265	7	S64938	hypothetical prote
22	41	42.7	410	7	T51212	8
23	41	42.7	720	7	T38647	hypothetical prote
24	41	42.7	742	7	T23226	ical prot
25	41	42.7	805	7	C88628	W03G1
56	41	42.7	805	~	C88037	protein K02E7.3 [i
27	41	42.7	805	7	T03896	hypothetical prote
28	41	42.7	906	7	T48898	
29	41	42:7	908	~	T48899	disease resistance

E2 glycoprotein pr	E2 glycoprotein pr	E2 glycoprotein pr	protein C17B7.7 [i	DNA strand transfe	186K protein - cuc	utrophin - human	hypothetical prote	16S rRNA processin	hypothetical prote	probable membrane	probable heat shoc	conserved hypothet	hypothetical prote	meiosis specific p	synaptic vesicle p
S14940	S14939	S07421	D88996	S13743	WMTMS2	S28381	H84010	A97759	F71691	F69972	T00825	AH0482	T06727	T43222	A43344
~	~	7	N	7	-	٦	7	~	~	~	0	~	N	~	-
1162	1162	1162	1217	1528	1646	3433	78	165	165	218	244	398	497	607	742
42.7	42.7	42.7	42.7	42.7	42.7	42.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7
41	41	41	41	41	41	41	40	40	40	40	40	40	40	40	40
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Surface glycoprotein CD59 precursor (validated) - human N;Alternate names: 1F5 antigen protein; 20K homologous restriction factor (HRF20); CD59 plex inhibition factor (MACIF); membrane inhibitor of reactive lysis (MIRL); protectin C;Species Homo sapiens (man) Bequence revision 30-Sep-1990 #text_change 09-Jul-2004 C;Accession: A46252; Jul109; A33405; Jul134; A34587; S05504; S09201; A60828; PL0041; A60 Rice Natl. Acad. Sci. U.S.A. 89, A876-7879, 1992 A;Fitenov. DE.; Sykes, K.; Kaufman, R.E.; Rosse, W.F. Proc. Natl. Acad. Sci. U.S.A. 89, A876-7879, 1992 A;Fitenove of the CD59-encoding gene: further evidence of a relationship to muri A;Reference number: A46252; MUID:92390353; PMID:1381503

A; Accession: A46252

A; Molecule type: DNA
A; Residues: 1-128 <-PET>
A; Residues: 1-128 <-PET>
A; Residues: 1-128 <-PET>
A; Residues: 1-128 <-PET>
A; Cross-references: UNIPROT: P13987; GB: M84349; GB: M82840; NID: g180149; PIDN: AAA88793.1;
A; Cross-reference extracted from NCBI backbone (NCBIN: 112714, NCBIN: 112718, NCBIN: 112720, R; Davies, A.; Simmons, D.L.; Hale, G.; Harrison, R.A.; Tighe, H.; Lachmann, P.J.; Waldma A; Exp. Med. 170, 637-654, 1989
A; Title: CDS9, an LY-6-1ike protein expressed in human lymphoid cells, regulates the act A; Accession: JL0109; MUID: 89361238; PMID: 2475570

A; Molecule type: mRNA A; Residues: 1-128 cDAV. A; Residues: 1-128 cDAV. A; Cross-references: EMBL:X16447; NID:929805; PIDN:CAA34467.1; PID:929806 R; Okada, H;; Nagami, Y; Takahashi, K.; Okada, N.; Hideshima, T.; Takizawa, H.; Kondo, J B; Ochem: Biophywa: Res. Commun. 162, 1553-1559, 1989 A; Title: 20 KDa homologous restriction factor of complement resembles T cell activating A; Reference number: A33405; MUID:89350983; PMID:2475111

A; Accession: A33405

A;Molecule type: mRNA A;Residues: 1-128 <OKA> A;Cross-references: GB:M27909; NID:g623406; PIDN:AAA60543.1; PID:g623407 R;Sugita, Y.; Tobe, T.; Oda, E.; Tomita, M.; Yasukawa, K.; Yamaji, N.; Takemoto, T.; Puz J. Biochem. 106, 555-557, 1989

A. Title: Molecular cloning and characterization of MACIF, an inhibitor of membrane chann A. Reference number: JU0134, MUID:90110046, PMID:2606909 A. Accession: JU0134

A; Molecule type: mRNA A; Residues: 1-128 <SUG> A; Note: parts of this sequence, including the amino end of the mature protein, were conf A; Note: parts of this sequence, including the amino end of the mature protein, were confirmed A; Note: sites for glycosylation and the absence of glycosylation were confirmed R; Sawada, R.; Ohashi, K.; Anaguchi, H.; Okazaki, H.; Hattori, M.; Minato, N.; Naruto, M. DMA Cell Biol. 9, 213-220, 1990 A; Title: Isolation and expression of the full-length cDNA encoding CD59 antigen of human A; Reference number: A34587; MUID:90253615; PMID:1692709

A, Residues: 1-128 <SAW>

A;Cross-references: GB:M34671; NID:g180152; PIDN:AAA51952.1; PID:g180153 R;Sawada, R.; Ohashi, K.; Okano, K.; Hattori, M.; Minato, N.; Naruto, M. Nucleic Acids Res. 17, 6728, 1989

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F;26-102/Domain: Ly-6 homology <LY6>
F;103-128/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;103-128/Domain: carboxyl-terminal propeptide #status experimental
F;28-51, 31-38, 44-64/Disulfide bonds: #status experimental
F;38/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;37/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;70-88, 89-94/Disulfide bonds: (or 70-89, 88-94) #status experimental
F;102/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature form)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: 136914
R;Fodor, W.L.; Rollins, S.A.; Bianco-Caron, S.; Burton, W.V.; Guilmette, E.R.; Rother, R Immunogenetics 41, 51, 1995
A;Title: Primate terminal complement inhibitor homologues of human CD59.
A;Reference number: 136894; MUID:95104908; PMID:7528724
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C;Superfamily: Ly-6 antigen; Ly-6 homology
F;26-102/Domain: Ly-6 homology <LY6>
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C;Superfamily: Ly-6 antigen; Ly-6 homology
F;26-100/Domain: Ly-6 homology <LY6>
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R;Fodor, W.L.; Rollins, S.A.; Bianco-Caron, S.; Burton, W.V.; Guilmette, E.R.; Rother, R Immunogenetics 41, 51, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2059 protein - green monkey
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Papio sp. (baboon)
C;Date: 07-Jun_1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
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F;26-102/Product: surface glycoprotein CD59 #status experimental <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-126 <RES>
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FANCNFNDISTLLKESE
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Matches 10; Conserv
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                                     A Mesterent manner: 505504; WIDL 53386003; PMID: 47518

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A,Title: Complementary DNA sequence and deduced peptide sequence for CD59/MEM-43 antigen
A,Reference number: S05504; MUID:89386002; PMID:2476718
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RESULT

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A;Cross-references: UNIPROT:Q915M0; GB:AE004506; GB:AE004091; NID:g9946584; PIDN:AAG0409 A;Experimental source: strain PAO1 C;Genetics: A;Gene: PAO708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete ganome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: E83748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q9XERO; GB:AP001509; GB:BA000004; NID:g10173176; PIDN:BAB045
A;Experimental source: strain C-125
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C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: O2-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB0002
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davies, P.; Dougan, G.; I.M.; Rittherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein BH0789 [imported] - Bacillus halodurans (strain C-125)
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                                                                                                                                                                                                                                                  3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 45; DB 2;
Pred. No. 27;
4; Mismatches
                                                                                                                                                                               Score 46; DB 2;
Pred. No. 7.2;
3; Mismatches
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136 FKHSNFHDYLTQIKE 150
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Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                               Query Match
Best Local Similarity 60.0%;
Matches 9; Conservative
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HCVPSNITTRLRELE 40
                                                                                                                                                                                                                                                                                                            3 HCNFNDVTTRLRENE 17
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CHINEMTTLIREN 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-777 <STO>
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A,Molecule type: DNA
A,Residues: 1-706 <KUR>
A;Residues: 1-284 <STO>
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20766
R;Palmer, S.
submitted to the EMBL Data Library, September 1995
A;Reference number: Z19321
A;Reference number: Z19321
A;Refatus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1767 < WIL.
A;Residues: 1-1767 < WIL.
A;Residues: 1-1767 < WIL.
A;Experimental source: clone F11C1
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probable transcription regulator PA0708 [imported] - Pseudomonas aeruginosa (strain PA01) c; Species Pseudomonas aeruginosa
C; Species Pseudomonas aeruginosa
C; Decises Pseudomonas aeruginosa
C; Decises Pseudomonas aeruginosa
C; Decises Pseudomonas aeruginosa
C; Decises Pseudomonas aeruginosa (strain PA01)
C; Accession: E83557
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradan, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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A,Accession: E83557
A,Status: preliminary
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-1302 <WIL>
A;Cross-references: UNIPROT:Q19346; EMBL:Z54270; PIDN:CAA91031.1; GSPDB:GN00028; CESP:F1
A;Experimental source: clone F11C1
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A;Introns: 21/1; 97/3; 134/3; 189/3; 245/3; 284/3; 474/2; 553/3; 701/2; 734/3; 807/1; 88
9/3; 1659/3; 1700/2
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A;Introns: 21/1; 97/3; 134/3; 189/3; 245/3; 284/3; 474/2; 553/3; 701/2; 734/3; 807/1;
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                         hypothetical protein F11C1.5b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Aate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20767
R;Palmer, S.
submitted to the EMBL Data Library, September 1995
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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Best Local Similarity
Matches 12; Conserva
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R;Cavanagh, D.; Davis, P.J.
Arch. Virol. 130, 471-476, 1992
A;Title: Sequence analysis of strains of avian infectious bronchitis coronavirus isolated
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A; Residues: 1-544 <CAV>
A; Residues: 1-544 <CAV>
A; Cross-references: UNIPROT: 082667; EMBL: X64737; NID: 9453158; PIDN: CAA46003.1; PID: 945315;
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1992
C; Superfamily: coronavirus E2 glycoprotein
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A;Experimental source: clone F09C6
                         A;Cross-references: UNIPROT:027791; GB:AE000931; GB:AE000666; NID:g2622885; PIDN:AAB8622
A;Experimental source: strain Delta H
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C;Species: avian infectious bronchitis virus, IBV
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004
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A;Accession: S41626
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA...
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Cibate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
CiAccession: T20652; T26370
R;Mortimore, B.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19305
A;Reference number: Z19305
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A;Molecule type: DNA
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Best Local Similarity 75.0%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches
                                                                                                                                                                                                              45.8%; Score 44; DB ilarity 53.3%; Pred. No. 45; Conservative 3; Mismatches
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Matches 8; Conserv
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A; Residues: 1-365 <WIL>
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   AMTH>
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                                                                                         C;Genetics:
A;Gene: MTH1763
A;Start codon: TTG
A, Residues: 1-807
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D69102
collagenase - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
A;Thile: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: D69102
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                      hypothetical protein F23A7.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T21283
R;McMurray, A.
R;McGession: T21283
A;Reference number: Z19401
A;Accession: T21283
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Mclecule type: DNA
A;Mcsedues: 1-1307 < WIL.>
A;Residues: 1-1307 < WIL.>
A;Experimental source: clone F23A7
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A,Experimental source: strain Madrid E
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: CESP:F23A7.5
A;Map position: X
A;Introns: 154/1; 230/2; 271/1; 307/1; 466/2; 551/2; 627/3; 663/1; 699/3; 746/3; 772/3;
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C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C;Accession: H71639
C;Accession: H71639
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499; PMID:9823893
A;Accession: H71639
A;Accession: H71639
A;Accession: L71630; MUID:99039499; PMID:9803893
A;Accession: L71639
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H71639
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain J RP790 - Rickettsia prowazekii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
A;Gene: nuoJ; RP790
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 6
C;Keywords: membrane-associated complex; NAD; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 45; DB 2;
Pred. No. 52;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.9%;
69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      654 CKINDDTTILREN 666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 66.7
Matches 8; Conservative
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NFNQAITKLREN 88
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Riglaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.
Jounnguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                     RESULT 14
ABC transporter (substrate-binding protein) BH0251 [imported] - Bacillus halodurans (str
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Date: 01-Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q9KG62; GB:AP001507; GB:BA000004; NID:g10172612; PIDN:BAB035
A;Experimental source: strain C-125
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AB1326
hypothetical protein lmo2013 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Dec-2002
C;Accession: AB1326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 43.8%; Score 42; DB 2; Length 419; Best Local Similarity 40.0%; Pred. No. 48; Matches 6; Conservative 6; Mismatches 3; Indels
                                6; Indels
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C;Superfamily: uncharacterized conserved protein
56.2%; Pred. No. 42; tive 1; Mismatches
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A,Gene: BH0251
C,Superfamily: LIV-binding protein
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                                                                                                                                           288 FEHLCFQDVKERLLES 303
                                                                                     1 FEHCNFNDVTTRLREN 16
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219 HTDYNTIISRIRESE 233
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Best Local Similarity 56.2
Matches 9; Conservative
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A;Molecule type: DNA
A;Residues: 1-419 <STO>
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A;Molecule type: DNA
A;Residues: 1-434 <GLA>
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Matches 9; Conserv
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8, 2005, 10:24:21 ; Search time 89.3488 Seconds (without alignments) 97.431 Million cell updates/sec
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-020-393B-3_COPY_42_58 96 1 FEHCNFNDVTTRLRENE 17 score: Sequence: Title: Perfect

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 200000000 Minimum

Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SIMMARIES

		do			SUMMARIES	
Result No.	Score	Ouery Match	Query Match Length	DB	ID	ription
7	96	100.0	! !	-	CD59 HUMAN	P13987 h cd59 glyc
7	63	65.6		Н	CDS9_PAPSP	papio s
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4	63	9:59		~	Q8SP <u>I</u> 3	
ഹ	9	62.5		~	Q8SQ46	Q8sq46 macaca fasc
9	51.5	53.6	337	~	Q7ZNX4	human i
۲	51	53.1	935	~	Q6FSB7	Q6fsb7 candida gla
æ	49	51.0	N	ч	CD59_RABIT	oryctol
6	49	51.0	128	Н	CD59 AOTTR	P51447 actus trivi
10	49	51.0	143	~	Q966 <u>T</u> 6	Q966t6 dictyosteli
11	48	50.0	48	~	Q8M8Z4	
12	48	50.0		~	Q27308	
13	47	49.0	128	Н	CDS9 CALSQ	
14	47	49.0		~	Q6BZR9	
15	47	49.0		N	081985	Q8i9s5 heterodera
16		48.4	1302	7	Q7JMA4	Q7jma4 caenorhabdi
17	46.5	48.4	~1	7	Q19346	
18	46	47.9	284	~	Q915M0	Q9i5m0 pseudomonas
19	46	47.9	338	Н	ARGC LEPIN	
20	46	•		~	Q9KER0	
21	46		93	~	Q8WZU8	Q8wzu8 neurospora
22	45	46.9	127	N	Q705Z7	
23	45	46.9		~	060080	Q8qq90 avian infec
24	45	46.9		~	Q7TAV1	Q7tav1 avian infec
25	45	46.9	165	~	Q68X25	Q68x25 rickettsia
56	45	46.9		~	Q6N8Z8	m
27	45			~	Q81L43	Q8il43 plasmodium
28	45	46.9	448	7	Q6BWL4	
59	45	46.9	23	~	Q6J1E2	
30	45	46.9	548	~	Q913Y3	Q913y3 avian infec
31	45	46.9	618	7	QBOMTS	Q80mt5 avian infec

MEDLINE-90253615; PubMed-1692709; Sawada R., Ohashi K., Anaguchi H., Okazaki H., Hattori M., Minato N.,

SEQUENCE FROM N.A.

32	45	46.9	706	8	Q664N9		yersinia ps
33	45	46.9	206	~	Q8ZJD9	Q8zjd9	yersinia pe
34	45	46.9	965	~	Q7Z1J6		caenorhabdi
35	44	45.8	84	7	Q8MNZ8		schistosoma
36	44		133	~	Q91SA9	091889	avian infec
37	44		136	7	Q91SB0		avian infec
38	44	45.8	205	Н	NUOJ RICPR	O9zcg3	rickettsia
39	44		202	~	Q68VV9		rickettsia
40	44	45.8	231	~	QSIFL1		plasmodium
41	44		236	7	091177	771160	avian infec
42	44		275	7	Q8CSS9	Q8C8B9	staphylococ
43	44		513	~	Q82618	082618	avian infec
44	44	45.8	530	~	055343	055343	avian infec
45	44	45.8	534	~	Q6J1D9	Q6j1d9	avian infec
					ALIGNMENTS		
ESULT 1 D59_HUMAN							

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MEDINE=90168959; PubMed=1689664;
Philbrick W.M., Palfree R.G.E., Roger G.E., Maher S.E., Bridgett M.M., Siriln S., Bothwell A.L.M.;
Siriln S., Bothwell A.L.M.;
"The CD59 antigen is a decibility homologue of murine Ly-6 antigens but lacks interferon inducibility.";
Eur. J. Immunol. 20:87-92(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "20 KDa homologous restriction factor of complement resembles T cell
                                                               01-JAN'-1990 (Rel. 13, Created)
01-JAN'-1990 (Rel. 13, Last sequence update)
25-GCT-2004 (Rel. 45, Last annotation update)
CDS9 glycoprotein precursor (Membrane attack complex inhibition effector) (MACIF) (MAC-inhibitory protein) (MACIF) (MACIF) antigen)
(Protectin) (Membrane inhibitor of reactive 19sis) (MTRL) (20 kDa homologous restriction factor) (HRF-20) (HRF-20) (1FS antigen).
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                                                                                                                                                                                                          Homo sapions (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                 MEDLINE=89361238; PubMed=2475570;
Davies A., Simmons D.L., Hale G., Harrison R.A., Tighe H.,
Lachmann P.J., Waldmann H.;
"CDS9, an LY-6-like protein expressed in human lymphoid cells,
regulates the action of the complement membrane attack complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90110046; PubMed=2606909; Sugita Y., Tobe T., Oda E., Tomita M., Yasukawa K., Yamaji N., Takemoto T., Furuichi K., Takayama M., Yano S.; "Molecular cloning and characterization of MACIF, an inhibitor membrane channel formation of complement."; J. Biochem. 106:555-557(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-89350983; PubMed-2475111;
Okada H., Nagami Y., Takahashi K., Okada N., Hideshima T.,
Takizawa H., Kondo J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activating protein.";
Biochem. Biophys. Res. Commun. 162:1553-1559(1989)
                                128 AA.
                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                       homologous cells.";
J. Exp. Med. 170:637-654(1989).
                                STANDARD;
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                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. TISSUE=T-cell;
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                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                CD59 HUMAN
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IDENTIFICATION OF COMPLEMENT INHIBITORY DOMAIN.
  KENDELINE=2238825; PubMed=12477832; DOI=10.1073/pnas.242603899;
KITAUSDE=2010115; P.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A. Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
B. M. Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
B. M. Butterfield A.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,
B. M. Butterfield A.S. N., Krzywinski M.I., Skalska U., Smailus D.E.,
B. M. Borden And Initial analysis of more than 15,000 full-length human
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MEDLINE=89386002; PubMed=2476718;
Sawada R., Ohashi K., Okano K., Hattori M., Minato N., Naruto M.;
"Complementary DNA sequence and deduced peptide sequence for CD59/MEM-43 antigen, the human homologue of murine lymphocyte antigen Ly-6C.";
Nucleic Acids Res. 17:6728-6728(1989).
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"Gene structure of human CD59 and demonstration that discrete mRNAs are generated by alternative polyadenylation.";
J. Mol. Biol. 227:971-976 (1992).
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                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=92390353; PubMed=1381503;
Petranka J.G., Fleenor D.E., Sykes K., Kaufman R.E., Rosse W.F.;
"Structure of the CD59-encoding gene: further evidence of a
relationship to murine lymphocyte antigen Ly-6 protein.";
Proc. Natl. Acad. Sci. U.S.A. 89:7876-7879(1992).
                         full-length cDNA encoding CD59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92317101; PubMed=1377690;
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                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93021133; PubMed=1383553;
                    "Isolation and expression of the antigen of human lymphocytes."; DNA Cell Biol. 9:213-220(1990).
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  Naruto M.;
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Tregulatory protein CD53.";

Tregulatory protein CD53.";

Structure of a soluble, glycosylated form of the human complement regulatory protein CD53.";

Structure 2.185-199 (1994).

Structure 2.185-199 (1994).

- I- FUNCTION: Potent inhibitor of the complement membrane attack complex (MAC) action. Acts by binding to the CB and/or C9 complements of the assembling MAC, thereby preventing incorporation of the multiple copies of C9 required for complete formation of the camolytic pore. This inhibitor appears to be species-specific. Involved in signal transduction for T-cell activation complexed to a protein tyrosine kinase. Interacts with T-cell surface antigen CD2.

--- SUBCELLULAR LOCATION' Attached to the membrane by a GPI-anchor.

---- PPW: N- and O-glycosylated. The N-gycosylation mainly consists of a family of bi-antennary complex-type structures with and without predominant O-glycans are mono-sialylated forms of the disaccharide, Gal-beta-1,3GalNAc, and their sites of attachment are probably on Thr-77.

---- PPW: Glycated Glycation is found in diabetic subjects, but only at minimal levels in nondiabetic subjects Glycated CD59 lacks which the complex of the disaccharidate of subjects of disactions of signal complexes of a complexed CD5 and the complexed CD59 lacks which the complexed CD59 lacks which the complexed CD59 lacks which complexes to vascular complications of disactions of complexed CD59 lacks which co
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                                                                                                                                                                                                                                                                                                                                                            STRUCTURE OF CARBOHYDRATES AND GPI-ANCHOR, AND SEQUENCE OF N-TERMINUS
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97207284; PubMed=9054419; DOI=10.1074/jbc.272.11.7229; Rudd P.M., Morgan B.P., Wormald M.R., Harvey D.J., van den Berg C.W., Davis S.J., Ferguson M.A., Dwek R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the complement regulatory protein CD59, a new cell-surface protein domain related to snake venom neurotoxins.";
Biochemistry 33:4471-4482(1994).
MEDLINE=97383147; PubMed=9235986; DOI=10.1021/bi9708321; Yu J., Dong S., Rushmere N.K., Morgan B.P., Abagyan R., Tomlinson S. Mapping the regions of the complement inhibitor CD59 responsible its species selective activity."; Biochemistry 36:9423-9428(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INHIBITION BY GLYCATION, AND MUTAGENESIS OF LYS-66 AND HIS-69.
MEDLINES-20266386; PubMed=10805801; DOI=10.1073/pnas.97.10.5450;
ACOSETA J., Hettinga J., Flueckiger R., Krumrei N., Goldfine A., Angarita L., Halperin J.;
"Molecular basis for a link between complement and the vascular complications of diabetes."
Proc. Omplications of Giabetes."
Proc. Natl. Acad. Sci. U.S.A. 97:5450-5455(2000).
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DATABASE: NAME=PROW; NOTE=CD guide CD59 entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd59.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94213818; PubMed=7512825;
Kieffer B., Driscoll P.C., Campbell I.D., Willis A.C.,
van der Merwe P.A., Davis S.J.;
"Three-dimensional solution structure of the extracell"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rthrocyte CD59.";
Biol. Chem. 272:7229-7244(1997)
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Length 126;

Score 63; DB 1;

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65.6%;
58.8%;
                                                            1 FEHCNFNDVTTRLRENE
                                                                             67 FANCNFNDISTLLKESE
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                               Conservative
                                                                                                                                                               STANDARD;
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128
102
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51
38
64
88
88
 Query Match
Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          assembly.
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                                                                                                                                                                                                                                                                  Name=CD59;
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SEQUENCE
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                                                                                                                                           CDS9_CERAE
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R HSSP; P13987; 1CDS.

B HSSP; P13987; 1CDS.

DR InterPro: IPR001526; LV6_UPAR.

DR Prom; PD003129; LJ-6_CD59; 1.

DR Prodom; PD003134; LJ, 1.

DR Prodom; PD003134; LJ, 1.

DR PROSTTE; PS00983; LV6 UPAR; 1.

RW Antigen; Glycoprotein; GPI-anchor; Lipoprotein; Signal.

FT SIGNAL

101 126 Removed in mature form (By similarity).

101 126 Removed in mature form (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95104908; PubMed=7528724;

MEDLINE=95104908; PubMed=7528724;

Guilmette E.R., Rother R.P., Zavoico G.B., Squinto S.P.;

"Primate terminal complement inhibitor homologues of human CD59.";

Immunogenetics 41.51-51(1995).

-!- FUNCTION: Potent inhibitor of the complement membrane attack complex (MAC) action. Acts at or after the C5b-8 stage of MAC
                                                                                                                                                                                                                                                                                                                         Papio sp. (Baboon).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
CDS9 glycoprotein precursor (Membrane attack complex inhibition factor) (MACIF) (MAC-inhibitory protein) (MAC-IP) (Protectin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-linked (GlcNAc. . .) (Potential) GPI-anchor amidated asparagine (By
                                                                          ö
                                            100.0%; Score 96; DB 1; Length 128; 100.0%; Pred. No. 4.1e-08;
                                                                         0; Indels
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By similarity.
By similarity.
By similarity.
By similarity.
No similarity.
                                                                                                                                                                                                          126 AA
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SIMILARITY: Contains 1 UPAR/Ly6 domain.
                                                                         Mismatches
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                                                                                                     1 FEHCNFNDVTTRLRENE 17
                                                                                                                        FEHCNFNDVTTRLRENE 83
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EMBL; X17198; CAA35059.1; -. EMBL; M34671; AAA51952.1; -.
                                                                         17; Conservative
                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                   Cercopithecinae; Papio.
NCBI_TaxID=61183;
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                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     assembly.
                                                                                                                                                                                                          CD59_PAPSP
                                                                                                                                                                                                                                                                                                          Name=CD59;
                                             Query Match
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CD59_PAPSP
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                                                                         Matches
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CD59 glycoprotein.

Removed in mature form (By similarity).

GP1-anchor amidated asparagine (By similarity).

UPAR/Ly6.

By similarity.

By similarity.
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                                     Gaps
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MEDLINE=55104908; PubMed=7528724;
ACOAT W.L., Rollins S.A., Bianco-Caron S., Burton W.V.,
Guilmette E.R., Rocher R.P., Zavoico G.B., Squinto S.P.;
"Primate terminal complement inhibitor homologues of human CD59.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunogenetics 41:51-51(1995).
-1- FUNCTION: Potent inhibitor of the complement membrane attack complex (MAC) action. Acts at or after the C5b-8 stage of MAC
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                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
CDS-9 glycoprotein precureor (Membrane attack complex inhibition factor) (MACIF) (MAC-inhibitory protein) (MAC-IP) (Protectin).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cercopithecus aethiops (Green monkey) (Grivet).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 128;
                                        Indels
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58.8%; Pred. No. 0.014;
tive 5; Mismatches
Pred. No. 0.014;
5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
-!- SIMILARITY: Contains 1 UPAR/Ly6 domain.
                                                                                                                                                                                                                                                                                                                                       128
                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P13987; 1CDS.
InterPro; IPR003632; Ly-6 CD59.
InterPro; IPR001526; LY6 UPAR.
Pfam; PF00021; UPAR_LY6; 1.
ProDom; P0003128; Ly-6_CD59; 1.
SWART; SM00134; LU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cercopithecinae, Cercopithecus.
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PROSITE; PS00983; LY6_UPAR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 N.
14007 MW;
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Gaps

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Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotā, Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mamadou S., Montavon C., Ben A., Djilo A., Rabiou S., Mboup S., Delaporte E., Peeters M., Dillo A., Rabiou S., Mboup S., Delaporte E., Peeters M., Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ429913; CAD22673.1; -.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019031; C:viral capsid; IEA.

GO; GO:0019031; C:viral envelope; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.
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                                                                                                                                                                                                                                                    62.5%; Score 60; DB 2; Length 128; 52.9%; Pred. No. 0.046;
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                                                                                                                                                                       128 AA; 14008 MW; 8867D956D63F6E52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QGFSB7;
05-UTL-2004 (TrEMBLrel. 27, Created)
05-UTL-2004 (TrEMBLrel. 27, Last sequence update)
05-UTL-2004 (TrEMBLrel. 27, Last annotation update)
Similar to sp|P40355 Saccharomyces cerevisiae YJR061w.
ORFNames=CAGL0H017939;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coat protein; Glycoprotein; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              935 AA.
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5; Mismatches
                                                                                                                                                                                                                                                                                                                                              6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
Pfam; PF00021; UPAR_LY6; 1.
ProDom; PD003128; Ly-6_CD59; 1.
SMART; SM00134; LU; 1.
PROSITE; PS00983; LV6 UPAR; 1.
SEQUENCE 128 AA; 14008 MW; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FEHCNFNDVTTRLRENE 17
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FRNCSFN-VTTELRDNK 45
                                                                                                                                                                                                                                                                                                                                                                                                                            1 FEHCNFNDVTTRLRENE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 FANCNYNDISTLLKESE 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
                                                                                                                                                                                                                                                                                               Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 58.8
Les 10; Conservative
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Q7ZNX4
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EMBL: AB072017; BAB86806.1; -. HSSP; P13987; ICDS.
HSSP; P13987; ICDS.
InterPro; IPR001526; LY6_UDAR.
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Bukaryota; Metacoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
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01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update) CD59 antigen p18-20 allele B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                   FEHCNFNDVTTRLRENE 17
                                                                                                  67 FANCNFNDISTLLKESE 83
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FANCNFNDISTLLKESE 83
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                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 21,
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TISSUE=Medulla oblongata;
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ProDom; PD003128; Ly-6_CD59; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhao X.-J., Zhao J., Zhou Q., Sims P.J.;
Identity of the residues responsible for the species-restricted complement inhibitory function of human CD59.";
J. Biol. Chem. 273:10665-10671 (1998).
-!- FUNCTION: Potent inhibitor of the complement membrane attack complex (MAC) action. Acts by binding to the C8 and/or C9 complements of the assembling MAC, thereby preventing incorporation of the multiple copies of C9 required for complete formation of the osmolytic pore.
--- SUBCELULAR LOCATION: Attached to the membrane by a GPI-anchor (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISCELLANEOUS: The mature form of this CD59 contains an additional serine residue before the conserved N-terminal leucine residue found in all other CD59 homologs sequenced to date.
SIMILARITY: Contains 1 UPAR/Ly6 domain.
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V., Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C., Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A., Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A., Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszul R., Lemaire M., Lowet P., Kachouri R., Nicaud J.M., Nikolaki M., Oztas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A., Swennen D., Tekaia F., Wesolowski-Louvel M., Westhoff E., Wirth B., Zeniou-Meyer M., Zlvanovic I., Bolotin-Fukuhara M., Thierry A., Michier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      077541;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
CD59 glycoprotein precursor (Membrane attack complex inhibition
factor) (MACIF) (MAC-Inhibitory protein) (MAC-IP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 25-64.
TISSUE=Erythrocyte, and Lymphocytes;
MEDLINE=98221206; PubMed=9553129; DOI=10.1074/jbc.273.17.10665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                    53.1%; Score 51; DB 2; Length 935; 52.9%; Pred. No. 13; ive 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                  Wincker P., Souciet J.L.;
"Genome evolution in yeasts.";
Mature 430:35-44(2004).
EMBL: CR380954; CAGS9810.1; -.
SEQUENCE 935 AA; 110737 MW; 5051C3B01DDB647F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 AA
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613 FNQDNFDDLSTRVRNNE 629
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InterPro; IPR001526; LY6 \overline{U}PAR.
Pfam; PF00021; UPAR_LY6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF040387; AAC23590.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FEHCNFNDVTTRLRENE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 52.9
nes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P13987; 1ERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity)
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                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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TODS9_RABIT
TODS9_RABIT
TODS9_RABIT
TOSS9_RABIT
TOSS9_R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                   form (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                               CD59 glycoprotein.
Removed in mature form (By similarity)
UPAR/LyG.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
N-linked (GlcNAC. . .) (Potential).
GPI_anchor_amidated glycine (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aotus trivirgatus (Night monkey) (Douroucouli).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fodor W.L., Rollins S.A., Bianco-Caron S., Burton W.V.,
Guilmette E.R., Rother R.P., Zavoico G.B., Squinto S.P.;
Frimate terminal complement inhibitor homologues of human CD59.";
Imwunogenetics 41:51-51(1995).
I- FUNCTION: Potent inhibitor of the complement membrane attack
complex (MAC) action. Acts at or after the C5b-8 stage of MAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2004 (Rel. 44, Last annotation update)
05-UUL-2004 (Rel. 44, Last annotation update)
CDS9 glycoproteal precursor (Membrane attack complex inhibition factor) (MACIF) (MAC-inhibitory protein) (MAC-IF) (Protectin).
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   SMART; SM00134; LU; 1.
PROSITE; PS00983; LV6_UPAR; FALSE_NEG.
Antigen; Direct protein sequencing; Glycoprotein; GPI-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.0%; Score 49; DB 1; Length 124; 50.0%; Pred. No. 3.1; tive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00134; LU; 1. TPROSITE; PS00983; LV6 UPAR; 1.
Antigen; Glycoprotein; GPI-anchor; Lipoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CEA64C816772CABD CRC64;
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-!- SIMILARITY: Contains 1 UPAR/Ly6 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity)
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Interpro; IPR001526; LY6 UPAR.
Pfam; PF00021; UPAR. LY6; 1.
Probom; PD003128; Ly-6 CD59; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 AA; 13870 MW;
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HSSP; P13987; 1CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FEHCNFNDVTTRLREN 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 YEDCNFEFISNRLEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                     Lipoprotein; Signal SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SM00134; LU;
SMART; SM00134; LU;
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Les 8; Conserv
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Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
Ericales; Styracaceae; Styrax.
                                                                                                                                                                                                                                                                                                   Bremer B., Bremer K., Heidari N., Erixon P., Olmstead R.G.,
Anderberg A.A., Kalbersjo M., Barkhordarian B.,
"Phylogenetics of asterids based on 3 coding and 3 non-coding
chloroplast DNA markers and the utility of non-coding DNA at higher
                                                                                                                             Last sequence update)
Last annotation update)
                                                                                     481 AA
                                                                                                                                                                                                                                                                                                                                                      Mol. Phylogenet. Evol. 24:273-300(2002).

Mol. Phylogenet. Evol. 24:273-300(2002).

EMBL; Ad-23300; CaD22196.1; --
GO; GO:0009507; C:chloroplast; IEA.
GO; GO:0008380; P:RNA splicing; IEA.
InterPro; IPR008998; Agglutinin.
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; Matk N.
Pfam; PF01348; Intron_maturas2; 1.
                                                                                                                 Created)
                                                                                     PRT;
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                                                                                                              01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.08;
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              55 CNFNELTOCFKENE 68
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Best Local Similarity 63.6
Matches 7; Conservative
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                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heat shock protein 82.
                                                                                                                                                           Maturase (Fragment).
                                                                                                                                                                                    Styrax officinalis.
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chloroplast.
                                                                                                                                                                         Name=matK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=hsp82
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                                                                                  08M8Z4
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                                                      RESULT 11
Q8M8Z4
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                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
By similarity.
CD59 glycoprotein.
Removed in mature form (By similarity).
UPAR/Ly6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=21541281; PubMed=11683919;
Aizawa H., Kishi Y., Iida K., Sameshima M., Yahara I.;
"Cofilin-2, a novel type of cofilin, is expressed specifically at aggregation stage of Dictyostellum discoideum development.";
Genes Cells 6:913-921 (2001).
                                                     By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
N-linked (GlcNAc. . .) (Potential).
GPI-anchor amidated asparagine (By
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                                                                                                                                                                                                Score 49; DB 1; Length 128;
Pred. No. 3.2;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baumgart C.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; ABOS52926; BAB62414.1; -.
EMBL; AC116984; AAOS1299.1; -.
                                                                                                                                                           similarity).
62D219B95589E55B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEOUENCE 143 AA; 16362 MW; A78731198E6F40B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Cofilin-2 (Hypothetical protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DictyBase, DDB0185192; cofc.
GO, GO:0005622; C:intracellular; IEA.
GO; GO:0003779; F:actin binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                       14200 MW;
                                                                                                                                                                                                                                                           1 FEHCNFNDVTTRLRENE 17
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Local Similarity 52.9%;
es 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 57.1%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=AX4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=DCOF3;
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                                       DOMAIN
DISULFID
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DISULFID
DISULFID
DISULFID
CARBOHYD
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SIGNAL
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STRAIN-Santa Tecla;
MEDLINE=96209490; PubMed=8630537;
Benedict M.Q., Levine B.J., Ke Z.X., Cockburn A.F., Seawright J.A.;
"Precise limitation of concerted evolution to ORFs in mosquito Hsp82
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=7167;
                                                                     .
0
                            Score 48; DB 2; Length 481;
Pred. No. 20;
3; Mismatches 1; Indels
481 AA; 56836 MW; 2BB62FBF8551A60F CRC64;
                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                  Anopheles albimanus (New world malaria mosquito).
                                                                                                                                                                                                                                      721 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Junect Mol. Biol. 5:73-79(1996).

EMBL; L47285; AABO5639.1; -.

EMBL; L47285; AABO5638.1; -.

HASSP; OO7900; LOSF.

GO; GO:0005524; F:ATP binding; IEA.
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DT
DT
DD
DD
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DB
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DB
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4 CNFNDVTTRLRENE 17

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NCBI_TaxID=284591;
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                               DISULFID
DISULFID
DISULFID
                                                                                           CARBOHYD
LIPID
                                                                                                                                                              SEQUENCE
           DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Callithrix sp. (Marmoset).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       By similarity.
CD59 glycoprotein.
Removed in mature form (By similarity).
UPAR/Ly6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95104908; PubMed=7528724;

MEDLINE=95104908; PubMed=7528724;

Podor W.L., Rollins S.A., Bianco-Caron S., Burton W.V.,

Guilmette E.R., Rother R.P., Zavoico G.B., Squinto S.P.;

Grilmette terminal complement inhibitor homologues of human CD59.";

Immunogenetics 41:51-51(1995).

I-FUNCTION: Potent inhibitor of the complement membrane attack

complex (MAC) action. Acts at or after the C5b-8 stage of MAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
CDS9 glycoprotein precursor (Membrane attack complex inhibition factor) (MAC-IP) (MAC-IP) (MAC-IP) (MAC-IP) (Protectin).
                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                         50.0%; Score 48; DB 2; Length 721;
43.8%; Pred. No. 31;
tive 5; Mismatches 4; Indels
GO; GO:0051082; F:unfolded protein binding; IEA.
GO; GO:0006485; P:protein folding; IEA.
GO; GO:0006986; P:response to unfolded protein; IEA.
InterPro; IPR003594; AFPbind_ATPase.
InterPro; IPR001404; Happ90.
Pfam; PF02518; HATPase c; 1.
Pfam; PF0218; HATPase c; 1.
PRINTS; PR00137; HATPase c; 1.
PRINTS; PR00137; HATPase c; 1.
PRINTS; PR00137; HATPase c; 1.
PROSITE; PS00298; HSP90; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003632; Ly-6 CD59.
InterPro; IPR001526; LY6 UPAR.
Pfam; PP00021; UPAR LY6; 1.
Prodom; PD0003128; Ly-6 CD59; 1.
SMART; SM00134; LU; LY6 UPAR; 1.
PROSITE; PS00983; LY6 UPAR; 1.
Antigen; Glycoprotein; GPI-anchor; Lipoprotein; Signal.
                                                                                                                                                                                                                                                                   721 AA; 82153 MW; C71867C5610452EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
-!- SIMILARITY: Contains 1 UPAR/Ly6 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              By similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                           455 EYCSLNDYVGRMKENQ 470
                                                                                                                                                                                                                                                                                                                                                                                                2 EHCNFNDVTTRLRENE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L22860; AAA35398.1; -.
                                                                                                                                                                                                                                                                                                                               43.8%;
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 43.0%
For 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26
103
26
28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD59 CALSQ
P46657;
                                                                                                                                                                                                                                             Heat shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=CD59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DISULFID
                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS9_CALSQ

ID CD59_CALSQ

TO 1-NOY.

DE CD59_CI

DE CD59_CI

SN Nameal.

OC Mammal.

OC MAmmal.

OC MAmmal.

RA MEDLINE

RA MEDLINE

RA MEDLINE

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RA FOGOL |

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                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
By similarity.
By similarity.
By similarity.
By similarity.
N'linked (GlCMAc. . .) (Potential).
GPI-anchor amidated asparagine (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
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                                                                                                                                                                                                                                                           Length 128;
                                                                                                                                                                                                                                                                                                                      6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; CR382132; CAG78906.1; -...
InterPro; IPR011009; Kinase_like.
InterPro; IPR000687; RIO1 UNK.
InterPro; IPR00058; Wing_hlx_DNA_bnd.
Pfam; PF01163; RIO1; 1.
SMART; SM00090; RIO; 1.
SEQUENCE 419 AA; 48198 MW; 660EC3BE22EE2622 CRC64;
                                                                                                                                                                                                   7A44CCAACDECEDD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-MINION SPIPALION Saccharomyces cerevisiae YNL207w.
ORFNames=YALIOF31383g.
Yarrowia lipolytica CLIB99.
                                                                                                                                                                                                                                                           49.0%; Score 47; DB 1; 47.1%; Pred. No. 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              419 AA.
                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 49.0%; Score 47; DB Best Local Similarity 50.0%; Pred. No. 25; Matches 7; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wincker P., Souciet J.L.;
"Genome evolution in yeasts.";
                                                                                                                                                                                                   128 AA; 14210 MW;
                                                                                                                                                                                                                                                                                                                                                                           1 FEHCNFNDVTTRLRENE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                67 FEDCTFROLSNOLSENE 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||:||:
226 HCDFNEFNIMIREN 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 HCNFNDVTTRLREN 16
                                                                                                                                                                                                                             Query Match
Best Local Similarity 4/...
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
  38
64
88
94
43
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Q819S5 PRELIMINARY; PRT; 721 AA.
Q819S5;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
H5P90.
H6Perodera glycines (Soybean cyst nematode)
H6Perodera; Metacoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.
NCBI_TAXID=51029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Stantar A.M., Carta L.K.;

Stantar A.M., Carta L.K.;

Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; AF461150; AA014563.2; -.

R HSSP; P079001; VER.

R GO; GO:0005524; F:ATP binding; IEA.

GO; GO:005524; F:ATP binding; IEA.

GO; GO:0056457; P:procein folding; IEA.

R InterPro; IPR003594; ATPbind_ATPase.

R InterPro; IPR003594; ATPbind_ATPase.

R InterPro; IPR003594; ATPBING_ATPASE.

R Pfam; PF00518; HATPase C: 1.

P Ffam; PF00718; HATPASE C: 1.

R PRMNS; PR00775; HEATPHOCK90.

R PRATT; SM00387; HATPASE C: 1.

R PROSITE; PS00298; HSP90; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49.0%; Score 47; DB 2; Length 721; 43.8%; Pred. No. 46; tive 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 43.8 nes 7; Conservative
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RESULT 15
10 281955
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AC 081995
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Search completed: June 8, 2005, 10:44:04 Job time : 92.3488 secs

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Gaps

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protein search, using sw model protein -Run on: δ

8, 2005, 12:14:04; Search time 159 Seconds (without alignments) 41.352 Million cell updates/sec

US-09-020-393B-3_COPY_42_58 96 score: Title: Perfect

FEHCNFNDVTTRLRENE 17 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

of hits satisfying chosen parameters: Total number

47

length: 0 length: 2000000000 DB seq DB seq Minimum I Maximum I Post-processing: Minimum Match 100% Maximum Match 100% Listing first 47 summaries

A_Geneseq_16Dec04: Database

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp1980s:* geneseqp1990s:*

geneseqp2003bs:*

geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Abb07534 Amino aci	Abb07537 Recombina	Aay27313 Human CD5	Abb07532 Human sol	Abb07535 Human rec	Abb07536 Human rec	Abb07540 Amino aci	Abb07538 Amino aci	Abb07539 Amino aci	Aaw09041 Human mem	Aar11426 Human lym	Aar32291 Sequence	Aam50629 Human CD5	Aar80239 Human mem		Aag03765 Human sec	Aag03764 Human sec	Ado41946 Human com	Aay27311 Human CD5	Aar04704 Sequence	Aar07444 Human mem	Aar11876 Human lym	Aar80240 Human mem	Aar86315 Human CD5	Aaw26318 Human CD5
SUMMARIES	8	ABB07534	ABB07537	AAY27313	ABB07532	ABB07535	ABB07536	ABB07540	ABB07538	ABB07539	AAW09041	AAR11426	AAR32291	AAM50629	AAR80239	AAG03766	AAG03765	AAG03764	AD041946	AAY27311	AAR04704	AAR07444	AAR11876	AAR80240	AAR86315	AAW26318
	DB	2	ß	~	2	S	ഹ	S	S	ß	7	~	7	ស	~	m	ო	m	œ	7	~	~	~	7	7	7
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÷	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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Humaa Humaa Humaa Humaa Humaa Humaa Humaa Humaa Humaa Humaa Humaa Humaa Pyo	Ada50058 P19 CTLA4 Ado41954 Human CD5 Ado41950 Human CR2
AAU00688 ADA50041 ADD55548 ADD55548 ADD455890 ADE58890 ADC59312 ADC95931 AAU00685 AAU00685 AAU00685 AAU0684 AAU0684 AAU51002 ADD50033 AAU5100684 AAU51000	ADA50058 ADO41954 ADO41950
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1288 1288 1288 1288 1288 1288 1288 1288	330
	100.0
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222288888888844444 37886011288888844444	4 4 4 7 4 7

ALIGNMENTS

ABB07534 standard; peptide; 70 AA.

ABB07534;

(first entry) 23-APR-2002

Amino acid sequence of APT634.

CD59; lipid raft derivative; DAF; neuroprotective; nootropic; human; cerebroprotective; antiparkinsonian; antialergic; antiulcer; cardiant; antiparkinatic; dermatological; hypotensive; vasotropic; antirheumatic; antiarkhitic; antilnilammatory; ophthalmological; immunosuppressive; antiarheumic; nephrotropic; antiinfertility;

immunosuppressive; antianemic; nephrotropic; ar antibacterial; antiatherosclerotic; vulnerary.

Homo sapiens.

WO200204638-A1.

17-JAN-2002.

06-JUL-2001; 2001WO-GB003034.

07-JUL-2000; 2000GB-00016811.

(ADPR-) ADPROTECH LTD

Ridley SH; Smith GP, Rowling PJE,

WPI; 2002-164646/21.

Lipid-raft targeted derivative of a soluble polypeptide e.g. a soluble complement regulatory molecule for treating disorders involving complement activity and various inflammatory, neurological and immune disorders.

Example 2; Page 44; 51pp; English.

The invention relates to a soluble derivative (I) of a soluble polypeptide. (I) has two or more heterologous membrane binding elements with low membrane affinity covalently associated with the polypeptide, the elements being capable of interacting with components of cellular or artificial membranes exposed to extracellular fluids and target lipid raft components of membrane. (I) is useful for treating disorders

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therapeutic agent, and for the preparation of a medicament for treatment to disorders and for the preparation of a medicament for treatment of disorders involving complement activity and various inflammatory and immune disorders. (I) is useful for treating neurological disorders (e.g. multiple solerosis, stroke, Parkinson's, Alzheimer's disease, traumatic brain injury and allergic encephalitis), disorders of inappropriate or undesirable complement activation (e.g. xenograft rejection, corneal graft rejection), inflammatory disorders (including ulcerative colitis, Crohn's disease, uveitis, psoriasis, asthma, scleroderma, acute pancreatits), post-isohaemic reperfusion conditions (e.g. myocardial infarction, hypertension, renal ischaemia, restenosis, atherosclerosis), infarctious diseases or sepsis (e.g. rheumatoid arthritis, systemic lupus erythematosus, haemolytic anemia, glomerulonephritis, and myssthemia
                                                                                                                                                                                                                                                                                                                                                                                                                                     gravis), reproductive disorders (antibody- or complement-mediated infertility), and wound healing. The present sequence represents the amino acid sequence of APT634, used in the synthesis of a lipid raft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 96; DB 5; Length 70; 100.0%; Pred. No. 1.9e-07; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid sequence of APT634, used in the synthesis of a
targeted derivative of soluble human urinary CD59 (APT637)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 70 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Local Similarity 100. Les 17; Conservative Best Loc Matches

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Gaps

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1 FEHCNFNDVTTRLRENE 17 FEHCNFNDVTTRLRENE 58 42 g à

ABB07537 standard; peptide; 71 AA. RESULT 2

ABB07537;

(first entry) 23-APR-2002

Recombinant human CD59 protein with C-terminal cysteine (APT2061).

cardiant; CD59; lipid raft derivative; DAF; neuroprotective; nootropic; human; cerebroprotective; antiparkinsonian; antiallergic; antiulcer; cardiant, antipsoriatic; antiasthmatic; dermatological; hypotensive; vasotropic; antiarthribic; antiarthmatic; antiarthmatic; antiarthmatic; nephrotropic; antiunleuppressive; antiantenic; nephrotropic; antininfertility; antibacterial; antiatherosclerotic; vulnerary ABB07537

IID ABB0

XXX

XXX

XXX

ABBC

XXX

XXX

CD5

KW CCFC

K

Homo sapiens

WO200204638-A1

17-JAN-2002.

06-JUL-2001; 2001WO-GB003034.

07-JUL-2000; 2000GB-00016811

(ADPR-) ADPROTECH LTD

Ridley SH; Smith GP, Rowling PJE,

WPI; 2002-164646/21.

Lipid-raft targeted derivative of a soluble polypeptide e.g. a soluble complement regulatory molecule for treating disorders involving complement activity and various inflammatory, neurological and immune

Example 7; Page 45; 51pp; English.

The invention relates to a soluble derivative (I) of a soluble polypeptide. (I) has two or more heterologous membrane binding elements with low membrane affinity covalently associated with the polypeptide,

the elements being capable of interacting with components of cellular or artificial membranes exposed to extracellular fluids and target lipid caft components of membrane. (I) is useful for treating disorders components of membrane. (I) is useful for treating disorders not the peptide fragment of CDS9, DAF or other the reapeutic agent, and for the preparation of a medicament for treatment of disorders involving complement activity and various inflammatory and immune disorders. (I) is useful for treating neurological disorders (e.g. multiple sclerosis, stroke, Parkinson's, Alzheimer's disease, traumatic complement activation (e.g. xenograft rejection, corneal complement activation (e.g. xenograft rejection, corneal crops disease, uveitis, psoriasis, asthma, scleroderama, acute pancreatitis), post-ischaemic repetfusion conditions (e.g. myocardial infarction, Mypertension, renal ischaemia, restenosis, atherosclerosis), infections diseases or sepsis (e.g. multiple organ failure, septic complement diseases (e.g. rheumatoid arthritis, systemic lupus erychematosus, haemolytic anemia, alomenulomephritis and myasthenia gravis), reproductive disorders (antibody- or complement-mediated infartility), and wound healing. The present sequence represents APT2061 which comprises soluble human CDSand a C-terminal oysteine residue, recombinantly expressed in chinese hamster ovary cells ö Compounds modulating CD59 mediated complement activity, for treatment of, e.g. immunovasculitis. The invention relates to compounds modulating CD59 mediated complement activity. It provides (i) molecules structurally mimicking human CD59 amino acid residues 42-58 (region which serves as binding site for CD59 Gaps CD59 mediated complement; human; Cd59 protein; C9 protein; mimetic; tumour therapy; complement-mediated inflammation; immune disorder; immunovasculitis; rheumatoid arthritis; scleroderma; C5b-9 complex; ö Score 96; DB 5; Length 71; Pred. No. 2e-07; Mismatches 0; Indels Disclosure; Fig 8A-B; 75pp; English AAY27313 standard; peptide; 77 AA. ; 1 FEHCNFNDVTTRLRENE 17 100.08; (OKLA-) OKLAHOMA MEDICAL RES (BLOO-) BLOOD CENT RES FOUND 100.08; 98US-00020393 99WO-US002802 Human CD59 protein fragment FEHCNFNDVTTRLRENE 05-NOV-1999 (first entry) Local Similarity 100. les 17; Conservative plasma membrane antiqen WPI; 1999-527301/44. Sequence 71 AA; 09-FEB-1998; 09-FEB-1999; Homo sapiens WO9940115-A2 12-AUG-1999 Query Match Sims PJ; Matches RESULT 3 AAY27313 엄 ò

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c9 interactions) when they are in a spatial orientation which can inhibit the formation of the human C5b-9 complex. These mimetics specifically bind to amino acid residues 359-384 of human C9. (ii) molecules structurally mimicking C9 amino acids 359-384 when they are in a spatial orientation which can promote the formation of the C5b-9 complex. Compounds that mimic CD59 can be used to increase CD59 inhibition of C5b-9 complex assembly. This is especially useful in patients in need of suppression of complement-mediated inflammation, e.g. immune disorders and diseases such as immunovasculitis, rheumatoid arthritis, scleroderma. Compounds that mimic C9 can be used to promote C5b-9 complex assembly. This is useful in patients in need of complement activation. The composition can be administered as an adjunct to tumour therapy. The present sequence represents a human CD59 (a plasma membrane antigen)
                                                                                                                                                                                                                                                                                                                                                                                                                              protein fragment
         8X969696969696888
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Query Match

Sequence 77 AA;

100.0%; Score 96; DB 2; Length 77; 100.0%; Pred. No. 2.1e-07; ive 0; Mismatches 0; Indels 1 FEHCNFNDVTTRLRENE 17 FEHCNFNDVTTRLRENE 17; Conservative Best Local Similarity Matches ઠે 윱

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RESULT

ABB07532

ABB07532;

ABB07532 standard; peptide; 77 AA.

(first entry) 23-APR-2002

Human soluble CD59 fragment

cerebroprotective; antiparkinsonian; antiallergic; antiulcer; cardiant; antipsoriatic; antiasthmatic; dermatological; hypotensive; vasotropic; antirtheritic; antiinflammatory; ophthalmological; immunosuppressive; antianemic; nephrotropic; antiinfertility; antianemic; nephrotropic; antiinfertility; antiatherosclerotic; vulnerary. CD59; lipid raft derivative; DAF; neuroprotective; nootropic; human;

Homo sapiens

WO200204638-A1.

17-JAN-2002

06-JUL-2001; 2001WO-GB003034.

07-JUL-2000; 2000GB-00016811.

(ADPR-) ADPROTECH LID.

Ridley SH; Rowling PJE, Smith GP,

WPI; 2002-164646/21.

Lipid-raft targeted derivative of a soluble polypeptide e.g. a soluble complement regulatory molecule for treating disorders involving complement activity and various inflammatory, neurological and immune disorders

Example 1; Page 43; 51pp; English.

The invention relates to a soluble derivative (I) of a soluble polypeptide. (I) has two or more heterologous membrane binding elements with low membrane affinity covalently associated with the polypeptide, the elements being capable of interacting with components of cellular or artificial membranes exposed to extracellular fluids and target lipid raft components of membrane. (I) is useful for treating disorders amenable to treatment by a soluble peptide fragment of CD59, DAF or other

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therapeutic agent, and for the preparation of a medicament for treatment of disorders involving complement activity and various inflammatory and immunity disperse involving complement activity and various inflammatory and immunity and allergic encephalitis), disorders of inappropriate or undesirable complement activation (e.g. xenograft rejection, conneal graft rejection), inflammatory disorders (including ulcerative colitis, conneating), post-ischaemic reperfusion conditions (e.g. mycardins), post-ischaemic reperfusion conditions (e.g. mycardins), infarction, renal ischaemia, restenosis, atherosclerosis), infarction, hypertension, renal ischaemia, restenosis, atherosclerosis), infarction, hypertension, renal ischaemia, restenosis, atherosclerosis), infarction, hypertension, renal ischaemia, restenosis, atherosclerosis), infectious diseases or sepsis (e.g. multiple organ failure, septic lupus erythematosus, haemolytic anemia, glomerulonephritis and myasthenia gravis), reproductive disorders (antibody- or complement-mediated fragment of soluble CDS9 isolated from human urine. This is used in the synthesis of a lipid raft targeted derivative of soluble human urinary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cerebroprotective; antiparkinsonian; antiallergic; antiulcer; cardiant; antiporiatic; antiathmatic; dermatological; hypotensive; vasotropic; antiathritic; antiinflammatory; ophthalmological; immunosuppressive; antianemic; nephrotropic; antiinfertility; antibacterial; antiatherosclerotic; vulnerary.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 96; DB 5; Length 77; 100.0%; Pred. No. 2.1e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB07535 standard; peptide; 82 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 77 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200204638-A1.
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                                                                                                                                                                                                                                                                                                                                                          CD59
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polypeptide. (I) has two or more heterologous membrane binding elements

with low membrane affinity covalently associated with the polypeptide, the elements being capable of interacting with components of cellular or artificial membranes exposed to extracellular fluids and target lipid raft components of membrane. (I) is useful for treating disorders amenable to treatment by a soluble peptide fragment of CD59, DAF or other the presparation of a medicament for treatment of disorders involving complement activity and various inflammatory and immune disorders. (I) is useful for treating neurological disorders (e.g. multiple sclerosis, stroke, parkinson's Alzheimer's disease, traumatic brain injury and allergic encephalitis) (disorders of inappropriate or undesirable complement activation (e.g. xenograft rejection, corneal complement activation (e.g. xenograft rejection, corneal complement activation (e.g. xenograft rejection, conneal complement activation (e.g. xenograft rejection, conneal complement activation (e.g. xenograft rejection, contitie, psoriasis, asthma, scleroderma, acute crown site of parcreatitis), post-ischaemic reperfusion conditions (e.g. myocardial infarction, hypertension, renal ischaemia, restenosis, atherosclerosis), infarction, hypertension, renal ischaemia, restenosis, atherosclerosis), infarction, hypertension, renal ischaemia, restenosis, atherosclerosis, confidentions diseases or sepsis (e.g. rheumatoid arthritis, systemic lupus continued isceases (e.g. rheumatoid arthritis, systemic lupus continued isceases (e.g. rheumatoid arthritis, and mysathemia

gravis), reproductive disorders (antibody- or complement-mediated infertility), and wound healing. The present sequence represents API which comprises coluble human CD59and a C-terminal cysteine residue, recombinantly expressed in B. coli

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ratificial membranes exposed to extracellular Hombonants of centural or after components of membrane. (1) is useful for treating disorders amenable to treatment by a soluble peptide fragment of CD59. DAF or other therapeutic agent, and for the preparation of a medicament for treatment of disorders involving complement activity and various inflammatory and ultiple sclerosis, stroke, Parkinson's Alzheimer's disease, traumatic brain injury and allergic encephalitis), disorders of inappropriate or undesirable complement activation (e.g. xenograft rejection, corneal cardin injury and allergic encephalitis), disorders of inappropriate or undesirable complement activation (e.g. xenograft rejection, corneal cardin a disease, uveitis, psoriasis, asthma, scleroderma, acute pancreatitis), post-ischaemic reperfusion conditions (e.g. myocardial infectious diseases or sepsis (e.g. multiple organ failure, septic shock), autoimmune diseases (e.g. multiple organ failure, septic erythem towns, haemolytic anemia, glomerulonephritis, systemic lupus cardin and mysasthenia
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elements being capable of interacting with components of cellular or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gravis), reproductive disorders (antibody- or complement-mediated infertility), and wound healing. The present sequence represents a
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Best Local Similarity
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Gaps

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Length 83; 0; Indels

Score 96; DB 5; 1 Pred. No. 2.3e-07; Mismatches

100.0%; 100.0%;

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17; Conservative

Query Match Best Local Similarity Matches 17; Conserv

Sequence 83 AA;

1 FEHCNFNDVTTRLRENE 17

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cerebroprotective, antiparkinsonian, antiallergic; antiulcer; cardiant, antiporiatic; antiasthmatic; dermatological; hypotensive; vasotropic; antirtheumatic; antiarthritic; antiinflammatory; ophthalmological; immunosuppressive; antianemic; nephrotropic; antiinfertility; antibacterial; antiatherosclerotic; vulnerary.
                                                                                                                                                                                                           CD59; lipid raft derivative; DAF; neuroprotective; nootropic; human;
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/note= "disulphide bridge"
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                                                                                 ABB07540 standard; peptide; 88 AA.
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                                                                                                                                                                             Amino acid sequence of APT2065.
 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUL-2000; 2000GB-00016811
43 FEHCNFNDVTTRLRENE
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Disulfide-bond
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                                                  RESULT 7
                                                                  ABB07540
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                                                                                               Lipid-raft targeted derivative of a soluble polypeptide e.g. a soluble complement regulatory molecule for treating disorders involving complement activity and various inflammatory, neurological and immune
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disorders.

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The invention (1) has two or more heterologous membrane binding elements with low membrane affinity covalently associated with the polypeptide, the elements being capable of interacting with components of cellular or artificial membranes exposed to extracellular fluids and target lipid cartificial membranes exposed to extracellular fluids and target lipid cartificial membrane by a soluble peptide fragment of CDS<sub>9</sub>. DAF or other components of membrane by a soluble peptide fragment of CDS<sub>9</sub>. DAF or other therapeutic agent, and for the preparation of a medicament for treatment of therapeutic agent, and for the preparation of a medicament for treatment of disorders involving complement activity and various inflammatory and immune disorders (1) is useful for treating neurological disorders (e.g. multiple sclerosis, stroke, Parkinson's, Alzheimer's disease, traumatic brain injury and allergic encephalitis), disorders of inappropriate or undesirable complement activation (e.g. xenograft rejection, corneal graft rejection), inflammatory disorders (including ulcerative colitis, Crohn's disease, uveitis, psoriasis, asthma, scleroderma, acute crohn's disease, uveitis, psoriasis, asthma, restenosis, atherosclerosis), infarctions diseases or sepsis (e.g. multiple organ failure, septic shock), autoimmune diseases (e.g. multiple organ failure, septic shock), autoimmune diseases (e.g. multiple organ failure, septic cromplementatosus, haemolytic anemia, glomerulomephritis and mysathenia cravis), reproductive disorders (e.g. rheumatoid arthritis, systemic lupus crythematosus, and wound healing. The present sequence represents the
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Lipid-raft targeted derivative of a soluble polypeptide e.g. a soluble complement regulatory molecule for treating disorders involving complement activity and various inflammatory, neurological and immune
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                                                                                                                  Example 8; Page 47; 51pp; English.
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hes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 88 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JAN-2002
                                                                         disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB07538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
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The invention relates to a soluble derivative (I) of a soluble polypeptide. (I) has two or more heterologous membrane binding elements of polypeptide. (I) has two or more heterologous membrane bindings capable of interacting with components of cellular or artificial membranes exposed to extracellular fluids and target lipid cartificial membranes of membrane. (I) is useful for treating disorders amenable to treatment by a soluble peptide fragment of CDS9. DAF or other the preparation of a medicament for treatment of disorders involving complement activity and various inflammatory and immune disorders. (I) is useful for treating neurological disorders (e.g. multiple sclerosis, stroke, Parkinson's, Alzheiner's disease, traumatic brain injury and allergic encephalitis), disorders of inappropriate or undesirable complement activation (e.g. xenograft rejection, corneal graft rejection), inflammatory disorders (including ulcerative colitis, Crohn's diseases or sepsis, sethma, scleroderma, acute pancreatitis), post-isfolemic reperfusion conditions (e.g. myocardial infarction, hypertension, renal ischemic restenois, atherosclerosis), infarctions diseases or sepsis (e.g. multiple organ failure, septic shock), autoimmune diseases (e.g. multiple organ failure, septic shock), autoimmune diseases (e.g. rheumatoid arthritis, systemic lupus erythematosus, haemolytic anemia, glomerulonephritis and myasthenia gravis), infaritity), and wound healing. The present sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD59; lipid raft derivative; DAF; neuroprotective; nootropic; human; cerebroprotective; antiparkinsonian; antiallergic; antiulcer; cardiant; antipsoriatic; antiasthmatic; dermacological; hypotensive; vasotropic; antirheumatic; antiarthritic; antiinflammatory; ophthalmological; immunosuppressive; antianemic; nephrotropic; antiinfertility; antiatherosclerotic; vulnerary.
                                                                                                                                           Lipid-raft targeted derivative of a soluble polypeptide e.g. a soluble complement regulatory molecule for treating disorders involving complement activity and various inflammatory, neurological and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 96; DB 5; Length 99; 100.0%; Pred. No. 2.8e-07; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83. .84
/note= "disulphide bridge"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                             Ridley SH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB07539 standard; peptide; 100 AA.
                                                                                                                                                                                                                                                      Example 8; Page 46; 51pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of APT2063.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid sequence of APT2062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FEHCNFNDVTTRLRENE 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
nes 17; Conservative
                                                             Rowling PJE, Smith GP,
                        (ADPR-) ADPROTECH LTD
                                                                                                      WPI; 2002-164646/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 99 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disulfide-bond
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                                                                                                                                                                                                               disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB07539;
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Matches
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WO200204638-A1.

17-JAN-2002

PJE,

Rowling

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The present sequence is the human membrane attack complex inhibitory factor (MACIF) mutant Asn18Gln (residues 1-77), which inhibits complement mediated cytolysis, and the release of FG12 and basic fibroblast growth factor (bFGF) by complement. It can be used to suppress transplanted organ rejection, especially hyperacute transplant rejection, and the nonlethal effects of complement, e.g. inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified human membrane attack complex inhibitory factor - has glutamine at position 18 and is an antiinflammatory and complement blocker, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lymphocyte; surface antigen; autoimmune disease; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yasunaga K, Itou K,
                                                                                                                                                                /note= "wild type Asn replaced by Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for inhibition of transplant hyper-acute rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 96; DB 2; 100.0%; Pred. No. 2.8e-07; ive 0; Mismatches 0;
                               1. .25
/label= sig_peptide
Location/Qualifiers
                                                                                                            /label= mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Egashira A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 35; 59pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human lymphocyte surface antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                (YAMA ) YAMANOUCHI PHARM CO LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 FEHCNFNDVTTRLRENE 83
                                                                                                                                                                                                                                                                                                                                                                                          95JP-00174282.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
                                                                                   .102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Suzuki H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-077527/07.
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                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                   13-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                          16-JUN-1995;
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                                                                                                                                                                                                                         WO9700320-A1
                                                                                                                                                                                                                                                                                03-JAN-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamaji N,
Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR11426;
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     Key
Peptide
                                                                                Peptide
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a soluble derivative (I) of a soluble pulpaperide. (I) has two or more heterologous membrane binding elements with Lub polypeptide. (I) has two or more heterologous membrane binding elements to be a soluble be a soluble being capable of interacting with components of cellular or artificial membranes exposed to extracellular fluids and target lipid raft components of membrane. (I) is useful for treating disorders of membrane by a soluble peptide fragment of CD59, DAF or other therapeutic agent, and for the preparation of a medicament for treatment of disorders involving complement activity and various inflammatory and immunity and allergic encephalitis), disorders of inappropriate or multiple sclerosis, stroke, Parkinson's, Alzheimer's disease, traumatic brain injury and allergic encephalitis), disorders of inappropriate or undeablabilable complement activation (e.g. xenograft rejection, corneal graft rejection), inflammatory disorders (including ulcerative colitis, Crohn's disease, uveitis, poortiasis, asthma, scleroderma, acute contents and c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infarction, hypertension, renal ischaemia, restenosis, atherosclerosis), infectious diseases or sepsis (e.g. multiple organ failure, septic shock), autoimmune diseases (e.g. rheumatoid arthritis, systemic lupus erythematosus, haemolytic anemia, glomerulonephritis and myasthenia gravis), reproductive disorders (antibody- or complement-mediated infertility), and wound healing. The present sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                       Lipid-raft targeted derivative of a soluble polypeptide e.g. a soluble complement regulatory molecule for treating disorders involving complement activity and various inflammatory, neurological and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human membrane attack complex inhibitory factor mutant Asn18Gln.
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                                                                                                                                                                                                                                                                                Ridley SH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW09041 standard; protein; 102 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Page 46; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid sequence of APT2063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FEHCNFNDVTTRLRENE 17
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                                                                                                            06-JUL-2001; 2001WO-GB003034
                                                                                                                                                                37-JUL-2000; 2000GB-00016811
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1es 17; Conservative
                                                                                                                                                                                                                                                                                Smith GP,
                                                                                                                                                                                                                         (ADPR-) ADPROTECH LTD
                                                                                                                                                                                                                                                                                                                                   WPI; 2002-164646/21.
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Gaps

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89JP-00183264.

14-JUL-1989;

23-SEP-1997

AAW09041;

Query Match Best Local S: Matches 17

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RESULT 10 AAW09041 Homo sapiens

(TORA) TORAY IND INC.

WPI; 1991-106290/15.

Length 102; Indels

Sugita Y;

Gape

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Length 103; Indels

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CD59; protectin; 1F-5Ag; H19; HRF20; MACIF; MIRL; P-18; human; genomics; evolution; AIDS; HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diseases or conditions such as unique or enhanced human brain functions, longer human life spans, susceptibility or resistance to disease, including AIDS and cancer, and aesthetic traits such as hair growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Determining human or non-human primate polynucleotide or polypeptide sequences associated with a physiological trait and have undergone evolutionary changes, for therapeutic use, involves using statistical
                Score 96; DB 2; I
Pred. No. 2.9e-07;
                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 18; Page 85-86; 141pp; English.
                                                                                                                                                                        AAM50629 standard; protein; 105 AA.
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                100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                       06-JUN-2001; 2001WO-US018310.
                               100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUN-2000; 2000US-00591435
                                                                     1 FEHCNFNDVTTRLRENE
                                                                                         FEHCUFNDVTTRLRENE
                                                                                                                                                                                                                                (first entry)
                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sikela JM;
Query Match
Best Local Similarity
Local 17; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-130744/17.
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                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                            Human CD59
                                                                                                                                                                                                    AAM50629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             methods
                                                                                                                                           RESULT 13
                                                                                                                                                         AAM50629
                                                                                             셤
                                                                                                                                                                                     à
                                                                                                                                                                                                                                                           ö
                                                                                                              This protein is similar to the murine lymphocyte antigen Ly 6. Antibodies raised against the antigen can be used in formulations for the treatment of autoimmune diseases, cancer and infections. The corresponding nucleotide sequence does not include an initial Leu codon. See also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The inventors claim a cell which contains a gene sequence which encodes protein CDS9.CDS9 is expressed by the cell and CDS9 inhibits complement mediated attack of the cell. The cells fail to elicit T lymphocyte mediated attack or are resistant to complement mediated attack. They can be used to treat patients with immune disorders. (Updated on 25-MAR-2003 to correct PN field.)
                                        Surface antigen of human lymphocyte - for use in study of human immune system of 101 residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetically engineered mammalian cell for treatment of coronary artery disease - inhibits complement-mediated attack and does not express surface proteins encoded by class I or II major histocompatability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bothwell ALM, Elliot EA, Flavell RA, Madri J, Rollins S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complement mediated attack inhibitor; CD59; transplant rejection; ss.
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                Length 103;
                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                             100.0%; Score 96; DB 2; I
100.0%; Pred. No. 2.9e-07;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                        AAR32291 standard; protein; 103 AA.
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                                                                                Claim 1; Page 1; 12pp; Japanese.
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92US-00906394.
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                                                                                                                                                                                                             Query Match
Best Local Similarity 10v.v..
                                                                                                                                                                                                                                                                                                     (revised)
(first entry)
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              N-PSDB; AAQ11251.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence of CD59.
                                                                                                                                                                                                  Sequence 103 AA;
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29-JUN-1992;
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08-JUN-1993
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RESULT 12 AAR32291 ID AAR

ઠે 셤 Length 105;

Score 96; DB 5; 1 Pred. No. 2.9e-07;

100.08;

Best Local Similarity

Query Match

Sequence 103 AA;

Bell

Gaps

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Matches

RESULT 14

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The present sequence is a polypeptide encoded by one of a large number of 5' ESTB derived from RNAs encoding secreted proteins. The 5' ESTB were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mENA because they are often obtained from oligo-dr primed cDNA libraries. Such ESTB are not well suited for isolating cDNA perimed cDNA libraries. Such ESTB are not well suited for isolating cDNA included. S' ESTB are derived from mENAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTB are derived from mENAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. S' ESTB are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expressed sequence tag; secreted protein; cDNA isolation;
(by SDS-PAGE) with a phosphatidylinositol (PI) anchor at position 76 (Glu) at the C-terminus. When the gene encoding MACIF is expressed in bacteria, the gene (see AAQ98521) gives a modified human MACIF protein comprising 128 amino acid residues (AAR80240); the PI anchor attachment does not occur in that case. (Updated on 25-MAR-2003 to correct PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNAs and genomic DNAs that correspond to 5'ESTs and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid that is a 5' expressed sequence tag (5' EST) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 96; DB 3; Length 115; 100.0%; Pred. No. 3.2e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 13; SEQ ID NO 7847; 71pp + Sequence Listing; English.
                                                                                                                                                                             Length 107;
                                                                                                                                                                                                                        Indels
                                                                                                                                                           Score 96; DB 2; Len
Pred. No. 3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein, SEQ ID NO: 7847.
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                                                                                                                                                                                                                                                                                                                                                                                                     AAG03766 standard; protein; 115 AA.
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                                                                                                                                                                                                                                                            1 FEHCNFNDVTTRLRENE 17
                                                                                                                                                                                                                                                                                                   83
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                                                                                                                                                                                 100.08;
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                                                                                                                                                                                                 Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI: 2000-500381/45.
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Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAC03772
                                                                                                                                          Sequence 107 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          also DNA and expression vectors used to regulate the complement system in the final stage of complement activation.

    .25
/label= secretory_signal_sequence
/note= "optionally not present, replaced with H or Met"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= PI anchor
/note= "modified by PI - skeletal structure composed of
phospho-ethanolamine, glycan and phosphatidylinositol"
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                                                                                                                                                                                                                                                                                                                                                          MACIF; membrane attack complex inhibition factor; complement system; regulation; activation; final stage; inhibit damage; disease therapy; type II allergy; inflammatory disease treatment; phosphatidylinositol anchor; glycoprotein; diagnosis.
      Gaps
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        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "core human MACIF protein"
                                                                                                                                                                                                                                                                                                                        Human membrane attack complex inhibition factor.
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      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                 AAR80239 standard; protein; 107 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 28; 49pp; English.
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                                          FEHCNFNDVTTRLRENE 17
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89JP-00247818.
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                                                                   FEHCNFNDVTTRLRENE
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      Conservative
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, Yano S,
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06-SEP-1989;
13-SEP-1989;
21-SEP-1989;
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                                                                                                                                                                                                                                                            25-MAR-2003
17-APR-1996
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      17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
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Protein

Peptide

Peptide

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Gaps

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AAG03765;

RESULT 16

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The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences fortived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can threfore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forenist, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
                                                                                      expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiinflammatory; dermatological; immunosuppressive; antiarthritic; antirheumatic; vasotropic; antidiabetic; neuroprotective; antiallergic; antiviral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement system; immunoconjugate; cancer; Hodgkin's lymphoma; myeloid leukaemia; hypoxic tumour; viral infection; inflammatory condition; rheumatoid arthritis; Crohn's disease; systemic lupus erythematosus; cytostatic; antiasthmatic; antiantimatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human; CD59; complement inhibitor; complement receptor 2; CR2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 96; DB 3; Length 115; 100.0%; Pred. No. 3.2e-07; ive 0; Mismatches 0; Indel8
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                                                                                                                                                                                                                                                                                                                                                                                                                                Duclert A, Giordano J;
                                            Human secreted protein, SEQ ID NO: 7845.
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                                                                                                                gene therapy; chromosome mapping
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06-OCT-2000 (first entry)
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Matches 17; Conservative
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                                                                                      5' EST;
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                                                                                                                                                          Homo sapiens
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                                                                                        Human;
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                                                                                                                                                                                                                                                                                                                                                        Human, S' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.
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Mismatches 0;
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                                                                                                                                                                                                                                                                                                                Human secreted protein, SEQ ID NO: 7846.
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                                                                                                                                                                   ,83
AAG03765 standard, protein, 115 AA.
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                                          67 FEHCNFNDVTTRLRENE 83
                     1 FEHCNFNDVTTRLRENE 17
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Best Local Similarity 100.
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AAG03764;

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RESULT 17

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AAG03764

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The invention relates to compounds modulating CD59 mediated complement activity. It provides (i) molecules structurally mimicking human CD59 anino acid residues 42-58 (region which serves as binding site for CD59 - C9 interactions) when they are in a spatial orientation which can inhibit the formation of the human C50-9 complex. These mimetics specifically bind to amino acid residues 359-384 of human C9. (ii) molecules exructurally mimicking C9 amino acids 359-384 when they are in a spatial crientation which can promote the formation of the C50-9 complex. Compounds that mimic CD59 can be used to increase CD59 inhibition of C50-0 complex assembly. This is especially useful in patients in need of suppression of complement-mediated inflammation, e.g. immune disorders and diseases such as immunovasculitis, rheumatoid arthritis, scleroderma. C0 compounds that mimic C9 can be used to promote C50-9 complex assembly. The composition can be administered as an adjunct to tumour therapy. The present sequence represents a human CD59 (a plasma membrane antigen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human 1F5 antigen; immunodiagnosis; pernicious anaemia;
rheumatoid arthritis; systemic lupus erythematosus; glomerular nephritis.
                                                                                                                                                                                                                                                       Compounds modulating CD59 mediated complement activity, for treatment of, e.g. immunovasculitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence of the 1F5 antigen derived from human cell membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 96; DB 2; Length 127; ilarity 100.0%; Pred. No. 3.6e-07; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR04704 standard; protein; 128 AA.
                                                                                                             RES FOUND.
                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 1A; 75pp; English.
                                                                                                                              BLOOD CENT RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FEHCNFNDVTTRLRENE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEHCNFNDVTTRLRENE 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88JP-00172187.
89JP-00129944.
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                                                                 98US-00020393.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89EP-00401996
                     99WO-US002802
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(first entry)
                                                                                                             OKLA-) OKLAHOMA MEDICAL
                                                                                                                                                                                                                         WPI; 1999-527301/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 127 AA;
                     09-FEB-1999;
                                                               09-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JUL-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JUL-1988;
23-MAY-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2003
30-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JAN-1990
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                                                                                                                                                                               Sims PJ;
                                                                                                                                (BLOO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR04704
ID AAR(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઢ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to novel targeted modulators of the complement receptor 2 (CR2) protein that is involved in regulating complement acceptor 2 (CR2) protein that is involved in regulating complement acceptor 2 (CR2) proteins that acceptor that has a complement inhibitor linked to the CR2, which can be used modulate the complement system i.e. the series of blood proteins that are major effectors of the immune system. The present invention describes compositions that can be used to treat various cancers including Hodgkin lymphoma, myeloid leukaemia and hypoxic tumours, viral infections such as herpes simplex virus, cytomegalovirus and paptein. Barr virus, as well as inflammatory conditions for example rheumatoid arthritis, Crohn's disease and systemic lupus erythematosus. Accordingly, these compositions exhibit cytostatic, antiasthmatic, antihiflammatory, dermatological, immunosuppressive, antiasthmatic, antihidemmatic, vasotropic, antidiabetic, neuroprotective, antiallergic, antihider and antiviral activities. This polypeptide sequence is the human complement inhibitor CD59 protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD59 mediated complement; human; Cd59 protein; C9 protein; mimetic; tumour therapy; complement-mediated inflammation; immune disorder; immunovasculitis; rheumatoid arthritis; scleroderma; C5b-9 complex;
                                                                                                                                                                                                                                                                                                                                                                                                        Composition useful for treating cancer, viral infection, bacterial infection, parasitic infection, inflammatory conditions, comprises construct having complement receptor 2 and modulator of complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 96; DB 8; I 100.0%; Pred. No. 3.5e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; SEQ ID NO 4; 184pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY27311 standard; peptide; 127 AA.
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                                                                                                                                                          13-NOV-2003; 2003WO-US036459.
                                                                                                                                                                                                      15-NOV-2002; 2002US-0426676P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human CD59 protein sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plasma membrane antigen.
                                                                                                                                                                                                                                                (MUSC-) MUSC FOUND RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                       WPI; 2004-420518/39.
                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ADO41945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 126 AA;
                                                                 WO2004045520-A2
                         Homo sapiens
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                                                                                                                                                                                                                                                                                             Comlinson S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-AUG-1999.
                                                                                                             03-JUN-2004
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                                                                                                                                                  the cell membrane fraction number of princytes which are configurating the cell membrane fraction suspended overnight in buffer config. 1% noty1-beta-D-glucopyranoside (NOG). After centrifugation, the supernatur is treated with solid (NH4)2SO4 to 60% satu. After centrifugation the paper. Is dissolved in buffer contg. 0.1%NOG, then dialysed overnight against the same plus 0.15 M NaCl. 1F5 antigen is a glycoprotein with a mol. wt. of 20-25 kD. It contains N-glycoside type carbohydrate chain and phosphatidylinositol. It inhibits complement-mediated cell membrane damage. It may be used to generate polyclonal or monoclonal antibodies (Abs) which may be used to determinine the presence of 1F5 antigen on the surface of erythrocytes, lymphocytes or other cells, thus enabling the systemic lupus erythematosus and glomerular nephritis. It may be used to treat disorders in which complement activation is involved. Abs to it may be used in targeting therapy, such as cancer cell lysis, or alimination of malignant cells. Residues 27-70 are encoded by a cDNA fragment of the gene which encodes 1F5 antigen prepad. by the polymerase chain reaction (in AAN93318). (Updated on 25-MAR-2003 to correct FR field.)
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                                                                                                                                         from human erythrocytes which are centrifuged and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human membrane attack complex inhibition factor (MACIF) gene product
5
                                                                   New glyco:protein IF5 antigen - derived from human cell membrane,
inhibits complement-mediated cell membrane damage.
Kondo
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                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 96; DB 2; Length 128; 100.0%; Pred. No. 3.6e-07; ive 0; Mismatches 0; Indels
Takizawa H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26. .128
/label= Mature MACIF protein.
Takahashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haemolysis; late complement components
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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89JP-00179933.
89JP-00230983.
89JP-00238246.
Okada N, Nagami Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FEHCNFNDVTTRLRENE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEHCNFNDVTTRLRENE 83
                                                                                                              Claim 3; p. 11; 26pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89JP-00281197.
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                                        N-PSDB; AAQ03116, AAN93318
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Best Local Similarity 100.
                                                                                                                                         Typically it is prepd.
                          WPI; 1990-016630/03
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-APR-1990;
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13-SEP-1989;
21-SEP-1989;
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28-JAN-1991
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12-JUL-1989;
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Okada H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
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                                                                                                                                                          Gene product may be expressed in large quantities and pure form from CHC cells, useful for inhibiting the activity of late complement components ie. haemolysis resulting from MAC formation. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Surface antigen of human lymphocyte - and gene and antibody useful for investigation and treatment of auto:immune disease, cancer, infection,
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                   Genes encoding protein with human MACIF activity - also expression vectors and proteins produced from expression of the genes.
                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                      100.0%; Score 96; DB 2; Length 128; 100.0%; Pred. No. 3.6e-07; tive 0; Mismatches 0; Indels
Takayama M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ly-6; cancer; autoimmune disease; pre A precursor.
Furuichi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26. .128
/label= Mature surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human lymphocyte surface antigen precursor

    .25
    label= Pre A precursor

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N-PSDB; AAQ11684, AAQ11685, AAQ11686.
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Takemoto T,
Yamaji N;
                                                                                                                                    Disclosure; Fig 1; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR11876 standard; protein; 128
                                                                                                                                                                                                                                                                                                                                    1 FEHCUFNDVTTRLRENE 17
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                                                                                                                                                                                                                                                                                                       Conservative
Sugita Y,
, Yano S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TORA ) TORAY IND INC
                                            WPI; 1990-322496/43
                                                                                                                                                                                                                                                                                    Local Similarity
tes 17; Conserv
                                                          N-PSDB; AAQ06262
                                                                                                                                                                                                                                          Sequence 128 AA;
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              rusakawa K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-JUL-1991
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 romita M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR11876;
                                                                                                                                                                                                                                                                      Query Match
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Matches
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Gaps

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Length 128; Indels

Score 96; DB 2; 1 Pred. No. 3.6e-07; Mismatches

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103. .128 /
/label= GPL anchor region
/hote= "GPL anchor region corresponds to amino acids 78-
103 of the mature CD59 protein"
                                                                                                                                                                                                                                                                                                                                                                                                      Terminal complement inhibitor protein; terminal CIP, CD59, CD46; transmembrane terminal CIP; TWTCIP; Ly6 antigen; transgenic animal; organ transplantation; glycosyl-phosphatidylinositol; GPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .25
/label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Squinto SP;
                                                                                                                                                                                                                                                        AAR86315 standard; protein; 128 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28. .96
/label= Ly6 motif
                                                   100.0%; FA
                                                                                                                    1 FEHCNFNDVTTRLRENE 17
                                             100.08;
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                                                                                                                                             67 FEHCNFNDVTTRLRENE
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                                                           Local Similarity 100.
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N-PSDB; AAT03338.
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Best Local Similarity
         Sequence 128 AA;
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                                                                                                                                                                                                                                                                                                                                 11-MAR-1996
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                                                                                                                                                                                                                                                                                                                                                                    Human CD59
                                                                                                                                                                                                                                                                                           AAR86315;
                                             Query Match
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                                                                                Matches
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                                                                  Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement system in the final stage of complement activation, and inhibite damage of human calls stage complement activation, and inhibite damage of human calls and tissues as a result of MAC formation. Naturally occuring human MACIF is a glycoprotein of mol. wt. 18 +/- 1 kba (by SDS-PAGE) with a phosphatidylinositol (PI) anchor at position 76 (Glu) at the C-terminus When the gene encoding MACIF is expressed in bacteria, the gene (see AAQ98532) gives a modified human MACIF protein comprising 128 amino acid residues (AAR80240); the PI anchor attachment field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide with human membrane attack complex inhibition factor activity also DNA and expression vectors used to regulate the complement system in the final stage of complement activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human membrane attack complex inhibition factor (MACIF) regulates the
                                                                                                                                                                                                                                                                                                                                                                                      MACIF; membrane attack complex inhibition factor; complement system; regulation; activation; final stage; inhibit damage; disease therapy; type II allergy; type II allergy; inflammatory disease treatment; phosphatidylinositol anchor; glycoprotein; diagnosis.
                                             Gaps
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/label= Pl_anchor_attachment_signal_sequence
         Length 128;
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                                             IndelB
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/label= secretory_signal_sequence
       Score 96; DB 2; I
Pred. No. 3.6e-07;
                                                                                                                                                                                                                                                                                                                                                  Human membrane attack complex inhibition factor.
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                                             Mismatches
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Yamaji N, Ito K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "human MACIF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                  AAR80240 standard; protein; 128 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 2; 49pp; English.
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89JP-00230983.
89JP-00238246.
       100.0%;
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                                                                                  FEHCNFNDVTTRLRENE 17
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                                                                                                      FEHCNFNDVTTRLRENE
                                                                                                                                                                                                                                                                                                               (first entry)
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                                             Conservative
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, Yano S,
                                                                                                                                                                                                                                                                                             (revised)
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N-PSDB; AAQ98532.
Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-JUL-1989;
06-SEP-1989;
13-SEP-1989;
21-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-APR-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP672683-A1
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                                                                                                                                                                                                                                                        AAR80240;
                                                                                                                      67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
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                                                                                                                                                                               RESULT
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Human CD59 (AAR86315) is a terminal complement inhibitor protein (CIP) that includes a C-terminal region involved in directing attachment of a glycosyl-phosphatidylinositol (GPI) anchor. A chimeric transmembrane terminal CIP (TWTCIP) comprising amino acids 1-77 of mature CD59 (i.e. lacking the GPI anchor region) and the transmembrane domain (amino acids expressed on the cell surfaces of the organs of transgenic animals. Such transgenic organs are protected from human complement attack upon
Terminal complement inhibitor chimeric protein and nucleic acid - esp against human complement, useful for protecting cells from complement attack e.g. in organ transplantation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 96; DB 2; | Pred. No. 3.6e-07;
                                                                                                                                                                                   Disclosure; Page 63-64; 85pp; English.
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Matches

셤 ò

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The sequence represents human CDS9 protein which is fused to human or porcine CTLA4 protein to form CTLA4-CDS9 chimeric protein. Chimeric proteins comprising a domain having CSb-9 and/or C3 inhibitory activity (e.g. CTLA4) and a domain having CSb-9 and/or C3 inhibitory activity (e.g. CTLA4) and a domain having T-cell inhibitory activity (e.g. CDS9) are capable of inhibiting both cellular immune responses and humoral immune responses. These polypeptides and their associated nucleic acids are useful for protecting pig cells of tissues and organs from both humoral and cellular rejection after xenotransplantation into humans. The sequences are capable of conferring resistance to humoral and cellular mechanisms of immune attack, to protect against human serum complement and to inhibit T-cell activation. Transgenic animals (for example, rodents, e.g. mouse, rati lagomorpha, e.g. rabbit, hare; and ungulates, e.g. pig, gat, sheep) expressing such a chimeric protein on the surfaces of their cells would have a higher chance of survival
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric protein useful for protecting xenotransplanted tissues by inhibiting cellular both humoral and immune responses, comprises a C5b-9 and/or C3 inhibitory domain, and a T-cell inhibitory domain.
                                                                                                                                                                               CTLA4; CD59; human; pig; T-cell activation; C5b-9 inhibitory activity; C3 inhibitory activity; cellular immune response; xenotransplantation; humoral immune response; human serum complement; rodent; mouse; rabbit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 96; DB 4; Length 128; 100.0%; Pred. No. 3.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                               rat; lagomorph; hare; ungulate; goat; sheep.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 2E(2); 51pp; English.
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                   AAU00688 standard; protein; 128 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0161186P.
                                                                                                                                                                                                                                                                                                                                                                                                            21-OCT-2000; 2000WO-US029151
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                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ALEX-) ALEXION PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fodor WL, Pizzolato M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-300497/31.
                                                                                                                                         Human CD59 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAS00682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 128 AA;
                                                                                                                                                                                                                                                                                                                           40200130966-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-OCT-1999;
                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                   07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                      03-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADA50041;
                                                           AAU00688;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C5b-9 protein. Claimed refroviral vector particles express a complement inhibitor such as CD59, and are thereby protected from inactivation upon exposure to body fluids containing complement. Also claimed are: (1) a producer cell producing the vector particle; and (2) a chimeric retroviral envelope protein (see also AAW26325) with at least part of the N-terminal receptor- binding domain removed and replaced by a protein domain having a complement inhibitor activity. The vector is used in a claimed method for transducing cells in the presence of a body fluid containing complement, preferably ex vivo, especially for gene therapy, e.g. of hereditary or acquired blood disorders by transduction of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Retroviral vector particle expressing complement inhibitor activity - for transducing cells in body fluids containing complement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This protein sequence comprises human CD59, an inhibitor of complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
  Gaps
                                                                                                                                                                                                                                                                                                                                                   CD59; MACIF; protectin; p18; human; C5b-9 complement inhibitor;
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  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                        retrovirus; vector; gene therapy; stem cell.
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Col 47-50; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .25
/label=_Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26. .128
/label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                               AAW26318 standard; protein; 128 AA
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                                        1 FEHCNFNDVTTRLRENE 17
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                                                               FEHCNFNDVTTRLRENE
                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            haematopoietic stem cells
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17; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAT84472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1994;
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                                                                                                                                                                                                                                                                17-NOV-1997
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                                                                                                                                                                                                                                                                                                          Human CDS9
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                                                                                                                                                                                                                          AAW26318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
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Gaps

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Human CD59 protein

Matches

8 유 RESULT 26

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Immunosuppressive; cellular immune response; humoral immune response;
cytotoxic T lymphocyte A4; CD152; CTLA4; CD59; xenotransplantation;
transplant rejection; human.
                                                                                                                                                                                                                                                                 New chimeric proteins comprising a first domain and a second domain capabale of inhibiting a cellular and humoral immune response, respectively, useful for regulating humoral and cellular effector functions of the immune system.

    .25
    /note= "Signal peptide"
    .128

                                                                                          /note= "Mature CD59"
                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                             Disclosure; Page 28; 59pp; English.
                                                                                                                                                                                                                      Fodor W;
                                                                                                                                              20-AUG-2002; 2002US-00225519,
                                                                                                                                                                10-AUG-2001; 2001US-00928267
                                                                                                                                                                                                                      Costa C, Pizzolato M,
                                                                                                                                                                                 (COST/) COSTA C. (PIZZ/) PIZZOLATO M.
                                                                                                                                                                                                                                       WPI; 2003-625623/59
                                                                                                                                                                                                    (FODO/) FODOR W.
                                                                                                                                                                                                                                               N-PSDB; ADAS0040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 128 AA;
                                                                                                            US2003086940-A1
                                      Homo sapiens
                                                                                                                             08-MAY-2003
                                                               Peptide
                                                                                 Protein
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The invention relates to a chimaeric protein comprising a first domain capable of inhibiting a cellular immune response and a second domain capable of inhibiting a humoral immune response. Also included are a chimaeric DNA construct (comprising a DNA sequence encoding a domain capable of inhibiting a bumoral immune response and a DNA sequence concerns of inhibiting a humoral immune response), a cloning vector comprising the DNA construct, a host cell transformed by the vector, a transgenic cell, tissue, organ or mammal comprising the chimaeric protein, producing a mammal, mammalian organ, tissue or cells, where the mammal is useful as an organ donor for a human or organ, tissue or cells chimaeric protein defined above into the mammal, organ, tissue or cells, where the protein defined above into the mammal, organ, tissue or cells, defined regions of the DNA appearing as ADASOO35 which encodes the pig CTLA4 (cytotoxic T lymphocyte A4, also known as CD152) and defined cefined cell after xenotransplantation into a human, and in inhibiting humoral and cellular immune response cells in a cregion, and human CD52 (humoral response region), and of CTLA4 and human cregions of cregions of the protein response region), and of CTLA4 and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   region) and human CD59 (humoral response region), and of CTLA.
DAF (not defined). The present sequence represents human CD59
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100.0%; Score 96; DB 7; Length 128; 100.0%; Pred. No. 3.6e-07; ive 0; Mismatches 0; Indels
                                                              1 FEHCNFNDVTTRLRENE 17
            Local Similarity 100.
 Query Match
                   Best Loca
Matches
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67 FEHCNFNDVTTRLRENE 83

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Gaps

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ADD25548 standard; protein; 128 AA.
RESULT 28
          ADD25548
ID ADD2
XX
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antiarthritic; immunosuppressive; antidiabetic; antithyroid;
neuroprotective; hinge region; immunoglobulin heavy chain;
CH2 constant region; CH3 constant region; 19G1;
antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
                            Binding domain-immunoglobulin fusion protein-associated protein #51.
                                                                            malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.
                                          Binding domain; immunoglobulin; fusion protein; cytostatic;
              15-JAN-2004 (first entry)
                                                                                                          Unidentified.
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Thompson PA; Hayden-Ledbetter MS, 25-JUL-2002; 2002US-00207655. 17-JAN-2001; 2001US-0367358P. 17-JAN-2002; 2002US-00053530. 03-JUN-2002; 2002US-0385691P. (GENE-) GENECRAFT INC WPI; 2003-801317/75. Ledbetter JA,

US2003118592-A1.

26-JUN-2003

New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.

Disclosure; SEQ ID NO 109; 157pp; English.

comprising a binding domain polypeptide that is fused to an immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain CH2 constant region polypeptide that is fused to the hinge region polypeptide, and an immunoglobulin heavy chain CH3 constant region polypeptide, and an immunoglobulin heavy chain CH3 constant region polypeptide that is fused to the CH2 constant region polypeptide comprises: a wild-type human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide derived from (a) having 3 or more cysteine residues; where the first cysteine is not mutated; a mutated human IgG1 immunoglobulin hinge region polypeptide contains 2 cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no more than one cysteine residue; and a mutated human IgG1 immunoglobulin hinge region polypeptide contains no more than one polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no cysteine residues. The binding domain-immunoglobulin fusion protein is capable of at least one immunological activity comprising antibody capable of at least one immunological activity comprising antibody dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The binding domain polypeptide is capable of specifically binding to an entire comprising the polymuclectide (operably linked to a promoter), a host cell transformed or transfected with a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein, a paramaceutical composition comprising the binding domain-immunoglobulin fusion protein, a pharmaceutical composition comprising the binding domain-immunoglobulin fusion protein or polymuclectide and a carrier, and treating a subject having or suspected of having a malignant condition or a B-cell disorder. The binding domain-immunoglobulin fusion protein is useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, cig. melanoma, carcinoma or sarcoma, rheumatoid arthritis, multiple sclerosis or autoimmune disease. The present sequence is a binding domain The invention relates to a binding domain-immunoglobulin fusion protein

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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the
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-immunoglobulin fusion protein-associated protein sequence. Note: The sequence data for this patent formed part of the printed specification and is also available in electronic format directly from USPTO at sequence.html?DocID=20030118592. The authors have not identified the sequences in the printed specification by their SEQ ID number therefore none of the sequences can be explicitly identified.
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, pain, neuronal tissue; gene therapy,
spinal segmental nerve injury; chronic constriction injury; CCI,
spared nerve injury; SNI; Chung.
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                                                                                                                                                                    Length 128;
                                                                                                                                                                                                    0; Indels
                                                                                                                                                                100.0%; Score 96; DB 7; I 100.0%; Pred. No. 3.6e-07;
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                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Protein NP_000602, SEQ ID NO 4782.
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                                                                                                                                                                                                                                                             FEHCHFNDVTTRLRENE 83
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26-NOV-2001; 2001US-0333347P
                                                                                                                                             Query Match
Best Local Similarity 100...
Local 17; Conservative
                                                                                                                                                                                                                                          FEHCNFNDVTTRLRENE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Woolf C, D'urso D,
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GENBANK; NP_000602.
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                                                                                                                                Sequence 128 AA;
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               pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polymuclectide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention discloses a composition comprising two or more isolated rat or human polymucleotides or a polymucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic polymucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polymucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptides, useful for
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specification, a method for identifying a compound useful in treating
                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chronic constriction injury; CCI;
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preparing a medicament for treating pain in an animal
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                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Protein NP_000602, SEQ ID NO 11194.
                                                                                                                                                                                    ftp.wipo.int/pub/published pct sequences
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spared nerve injury; SNI; Chung.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                                                                             17; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                      Sequence 128 AA;
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that increases or decreases the expression of the polymoleotide sequence that increases or decreases the expression of the polymoleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the activity of one or more of the compound that regulates the activity of one or more of the polymucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polympetides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polympetides or their antibodies. The polymucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene the sequence presented is a human protein (shown in Table 2 of the sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mitochondrial; human; screening assay; diabetes mellitus;
Huntington's disease; osteoarthritis;
Lieber's hereditary optic neuropathy; LHON;
mitochondrial nenephalopathy lactic acidosis and stroke; MELAS;
myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
osteopathic; ophthalmological; cytostatic.
         perform the method, an array, a method for identifying an agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human heat mitochondrial protein as a therapeutic target SeqID1118.
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Pred. No. 3.6e-07;
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100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ69312 standard; protein; 128 AA.
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17-JUN-2002; 2002US-0389987P.
20-SEP-2002; 2002US-0412418P.
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(BUCK-) BUCK INST AGE RES.
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Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-845369/78.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 128 AA;
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expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polymucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polymeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polymeptides or their antibodies. The polymucleotide or the compound that modulates its activity is useful for preparing a medicament for treating opin (e.g. spinal segmental nerve injury (Ctu) and spared nerve injury (Ctu) in an animal (e.g. gene the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 96; DB 7; Length 128; Best Local Similarity 100.0%; Pred. No. 3.6e-07; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Costigan M;
                                                                                                                                                                                                                                                                               specification, but was obtained in electi
ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human Protein NP_000602, SEQ ID NO 4778.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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GENBANK; NP_000602.
                                                                                                                                                                                                                                                                                                                                       Sequence 128 AA;
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Gaps

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Length 128; 0; Indels Glenn GM;

Taylor SW,

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                                                                                   for therapeutic intervention in treating adjease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERRE) or cancer. Accordingly, these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene; human; CD59; immune response inhibitor; xenotransplant rejection;
                                                                          invention relates to novel mitochondrial targets that can be used
comprises detecting a modified polypeptide in a sample and correlating
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                         compositions have neuroprotective, nootropic, antidiabetic, anticonvulsant, antiarchritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.
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100.0%; Pred. No. 3.6e-07;
iive 0; Mismatches 0;
                                           Claim 1; SEQ ID NO 1118; 180pp; English
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Best Local Similarity 100.
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(PIZZ/) PIZZOLATO M.
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N-PSDB; ADL91007.
                 with the disease.
                                                                                                                                                                                                                                                                                                                Sequence 128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2003157705-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-AUG-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human CD59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADL91008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADL91008
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The invention relates to a chimeric protein capable of inhibiting both cellular and humoral immune responses. The protein and DNA molecules are useful in the prevention or treatment of humoral and cellular rejection of xenotransplants. In particular, the DNAs may be used to produce

New chimeric protein capable of inhibiting both cellular and humoral immune responses, and DNA constructs encoding the chimeric protein, useful for preventing and/or treating rejection of xenotransplants.

Disclosure; Fig 2E2; 38pp; English.

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This invention relates to a method of differentially modulating the composition of blood endothelial cells (BEC) or lymphatic condothelial cells with a composition comprising an agent that differentially modulates blood or composition comprising an agent that differentially modulates blood or lymphatic endothelial cells. Treating hereditary lymphoedema comprises and entity a muteration in at correlates with lymphoedema and with a muteration in at least one allele of a gene encoding a LEC protein, where the mutation correlates with lymphoedema in human subjects, and with the proviso that composition comprising a lymphatic growth agent selected from VEGF-C or VEGF-D polypeptides and polymucleotides. The invention may be useful for the development of compounds with an antiangingenic, cytosteric, vasotropic or antininflammatory activity or for gene therapy. The method is useful in modulating the growth or differentiation of blood is useful in modulating the growth or differentiation of blood or an endothelial cells or lymphatic endothelial cells, in treating hereditary currently or for gene therapy. The method of a drug on endothelial cells. The agent is useful in manufacturing a medicament for the differential modulation of blood vessel endothelial cells or lymphatic vessel endothelial cell growth or differentiation. The lymphatic growth agent may also be used in manufacturing a medicament for lymphatic growth agent may also be used in manufacturing a medicament for
                                                                                                                                                                                                  ö
transgenic animals for use as tissue/organ donors, the cells of which are protected from human cellular immune responses due to their expression of the chimeric protein. The present sequence represents the amino acid sequence of human CD59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3; lymphatic growth agent; VEGF-C; VEGF-D; antianglogenic; cytostatic; vasotropic; antiinflammatory; gene therapy; endothelial cell disorder; inflammatory disease; cancer metestasis; lymphatic system; human.
                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saharinen J;
                                                                                                                                                       Length 128;
                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           growth; differentiation; blood endothelial cell; BEC;
                                                                                                                                                    100.0%; Score 96; DB 7; L
100.0%; Pred. No. 3.6e-07;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saharinen P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human BEC/LEC-related protein sequence SeqID855.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; SEQ ID NO 855; 176pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Petrova T,
                                                                                                                                                                                                                                                                                                                                                                                       ADN95931 standard; protein; 128 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                           1 FEHCNFNDVTTRLRENE 17
                                                                                                                                                                                                                                                                                  83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-MAR-2003; 2003WO-US006900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-MAR-2002; 2002US-0363019P.
                                                                                                                                                                                                                                                                  FEHCNFNDVTTRLRENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-2004 (first entry)
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alitalo K, Makinen T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LICENTIA LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-876899/81
                                                                                                                                                         Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ADN95932
                                                                                                                  Sequence 128 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                ADN95931;
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                                                                                                                                                                                                                                                                                                                                                RESULT 34
            8833333
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LEC gene or of other diseases involving the lymphatic vessels, such as various inflammatory diseases and cancer metastasis via the lymphatic system. The present sequence is that of a human LEC/BEC differentially expressed protein which is related to the method of the invention. Note: This sequence does not appear in the specification but was obtained by the indexer using the source data given in table 14 of the specification.
      treatment of hereditary lymphoedema resulting from a mutation in a
88888888888
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Sequence 128 AA;

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Gaps
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100.0%; Score 96; DB 7; Length 128; 100.0%; Pred. No. 3.6e-07;
                         Indels
                          ;
0
                          0; Mismatches
                                                     1 FEHCNFNDVTTRLRENE 17
                          17; Conservative
              Local Similarity
Query Match
              Best Loca
Matches
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67 FEHCNFNDVTTRLRENE 83

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ADP23084 standard; protein; 128 AA.
               polypeptide SEQ ID NO:178.
            (first entry)
            18-NOV-2004
        ADP23084;
RESULT 3:
ADP23084
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PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive; osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.

Unidentified

MO2004041170-A2

21-MAY-2004

30-OCT-2003; 2003WO-US034312.

01-NOV-2002; 2002US-0423394P

(GETH) GENENTECH INC.

Van Lookeren M, Williams PM, Clark H, Schoenfeld J,

Wood WI;

WPI; 2004-419628/39. Wu TD;

N-PSDB; ADP23083

New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral nervous system

Claim 7; SEQ ID NO 178; 2940pp; English.

antiathmatic, antiathmatic, and respiratory activity. A polymorlection of the invention may have a use in gene therapy. The PRO polypetide, its agonist, antagonist, or antibody that specifically binds to the expensive antagonist, or antibody that specifically binds to the polypeptide is useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, usunding arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mealitus, immune—mediated renal disease, a demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, The invention relates to a novel isolated nucleic acid and the PRO polypopetide encoded by it. A procein of the invention has antiinflammatory, antiarthritic, antitheumatic, immunosuppressive, osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Mnipple's disease, arythema multiforme, contact dermatitis, psoriasis, an allergic disease, asthma, allergic rhintits, atopic dermatitis, food hypersensitivity, urticaria, an immunologic disease of the lung, penemonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonia, idiopathic pulmonary fibrosis, hypersensitivity preumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, a transplantation associated disease, graft rejection or graft-versus-host disease. The present sequence represents a PRO protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                  Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human diagnostic and therapeutic pprotein SEQ ID NO:3350.
                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                    Score 96; DB 8; Pred. No. 3.6e-07;
                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABM83101 standard; protein; 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; Page; 190pp; English.
                                                                                                                                                                                                                                                                                100.0%;
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Suarez CJ;
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                                                                                                                                                                                                                                                                                                                                                                                              83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-SEP-2002; 2002US-0410259P.
                                                                                                                                                                                                                                                                                                                                                                                 67 FEHCNFNDVTTRLRENE
                                                                                                                                                                                                                                                                                                                                                             1 FEHCNFNDVTTRLRENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-329368/30.
N-PSDB; ACN41753.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kwong M, Pc
S, Shi X,
                                                                                                                                                                                                                 the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2004023973-A2.
                                                                                                                                                                                                                                                  Sequence 128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in gene mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-NOV-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABM83101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 36
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with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, dastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or gene therapy. The present sequence represents a dithp protein of the invention. Note: The sequence date for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Wang J;
Wang Z;
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            novel gene; novel protein; tissue marker; molecular weight marker;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel protein (useful for identifying genetic disorders) #132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhang J, Zhao QA,
ou P, Drmanac RT,
                                                                                                                                                                                                                                               100.0%; Score 96; DB 8; Length 130; 100.0%; Pred. No. 3.7e-07;
                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goodrich RW, Ren F, Zhang
weng G, Zhou P,
                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; SEQ ID NO 1043; 1177pp; English.
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Boyle BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome marker; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                       ADE07977 standard; protein; 190 AA
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Ghosh M, Xue AJ, Wehrman T, 1
Ma Y, Wang D, Chen R, Xu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-DEC-2001; 2001US-0339739P.
11-DEC-2001; 2001US-0339453P.
14-MAR-2002; 2002US-036591P.
14-MAR-2002; 2002US-0365384P.
12-APR-2002; 2002US-0372381P.
12-APR-2002; 2002US-037261SP.
22-APR-2002; 2002US-037261SP.
22-APR-2002; 2002US-0012858
                                                                                                                                                                                                                                                                                                                   1 FEHCNFNDVTTRLRENE 17
                                                                                                                                                                                                                                                                                                                                      FEHCNFNDVTTRLRENE 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                               Local Similarity 100.
nes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-569235/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ADE07066.
                                                                                                                                                                                                               Sequence 130 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
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                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rat; lagomorphs, e.g. rabbit, hare; and ungulates, e.g. pig, goat, sheep) expressing such a chimeric protein on the surfaces of their cells would have a higher chance of survival
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C2p-9
compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence represents a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                     CTLA4; CD59; human; pig; T-cell activation; C5b-9 inhibitory activity; C3 inhibitory activity; cellular immune response; xenotransplantation; humoral immune response; human serum complement; rodent; mouse; rabbit; rat; lagomorph; hare; ungulate; goat; sheep; mutant; mutein.
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric protein useful for protecting xenotransplanted tissues by inhibiting cellular both humoral and immune responses, comprises a and/or C3 inhibitory domain, and a T-cell inhibitory domain.
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                                                                                                                                      Indels
                                                                                                    Score 96; DB 7; I
Pred. No. 5.4e-07;
                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     Human CTLA4-human CD59 chimeric protein.
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                                                                                                                                                                                                                                                                                               AAU00685 standard; protein; 260 AA
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                                                                                                                                                                                             FEHCHFNDVTTRLRENE 145
                                                                                                                                                                          1 FEHCNFNDVTTRLRENE 17
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                                                                                                     100.08;
                                                                                                                      100.08;
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                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-300497/31.
N-PSDB; AAS00679.
                                                                                                     Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                  of the invention.
                                                                     Sequence 190 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                         129
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                                                                                                                                                                                                                                                                RESULT 38
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1 FEHCNFNDVTTRLRENE 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a chimaeric protein comprising a first domain capable of inhibiting a cellular immune response and a second domain capable of inhibiting a humoral immune response. Also included are a chimaeric DNA construct (comprising a DNA sequence encoding a domain capable of inhibiting a cellular immune response and a DNA sequence encoding a domain capable of inhibiting a humoral immune response by a construct a capable of inhibiting a humoral immune response of cloning vector comprising the DNA construct, a host cell transformed by the vector, a transgenic cell, tissue, organ or mammal comprising the chimaeric protein, producing a mammal, mammalian organ, tissue or cells, where the mammal is useful as an organ donor for a human or organ, tissue or cells chimaeric protein defined above into the mammal, organ, tissue or cells, where the protein is expressed in the mammal, organ, tissue or cells, where the protein is expressed in the mammal, organ, tissue or cells, where the protein is expressed in the mammal, organ, tissue or cells,
                                                                                                                                                                                          Immunosuppressive, cellular immune response, humoral immune response, cytotoxic T lymphocyte A4; CD152; CTLA4; CD59; xenotransplantation; transplant rejection; human; pig.
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New chimeric proteins comprising a first domain and a second domain capabale of inhibiting a cellular and humoral immune response, respectively, useful for regulating humoral and cellular effector functions of the immune system.
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  Indels
                                                                                                                                                                                                                                                                                                                                                             /note= "Synthetic (Asn-Ser)3 linker"
                                                                                                                                                                                                                                                                                                                  /note= "Human CD59 leader peptide"
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 Mismatches
                                                                                                                                                                     Pig CTLA4/human CD59 chimaeric protein #2.
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                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     'note= "Human CD59"
                                                                                                    ADA50035 standard; protein; 260 AA.
                                                                                                                                                                                                                                                                                                                                       "Pig CTLA4"
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                                  FEHCHFNDVTTRLRENE 215
                      FEHCUFNDVTTRLRENE 17
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                                                                                                                                                                                                                                                                                                                                                   .157
                                                                                                                                                                                                                                                                                                                                                                         .260
                                                                                                                                               (first entry)
 Conservative
                                                                                                                                                                                                                                                                                                                               .151
                                                                                                                                                                                                                                                                                                                                        /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COSTA C.
PIZZOLATO M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FODOR W.
                                                                                                                                                                                                                                                  Synthetic.
Homo sapiens.
Sus scrofa.
                                                                                                                                               20-NOV-2003
17;
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                                            199
                                                                                                                          ADA50035;
                                                                                                                                                                                                                                      Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (COST/)
                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (FODO/)
                                                                                                                                                                                                                                                                                                        Peptide
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  Matches
                                                                              RESULT 39
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cTLA4 (cytotoxic T lymphocyte A4, also known as CD152) and defined regions of the CTLA4 protein ADA50037. The chimaeric protein is useful in the protection of the porcine cell after xenotrangplantation into a human, and in inhibiting humoral and cellular defence mechanism. Chimaeras were produced comprising pig CTLA4 (cellular immune response region) and human CD59 (humoral response region), and of CTLA4 and human DAF (not defined). The present sequence represents a CTLA4/CD59 chimaera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a chimeric protein capable of inhibiting both cellular and humoral immune responses. The protein and DNA molecules are useful in the prevention or treatment of humoral and cellular rejection of xenotransplants. In particular, the DNAs may be used to produce transgenic animals for use as tissue/organ donors, the cells of which are protected from human cellular immune responses due to their expression of the chimeric protein. The present sequence represents the amino acid sequence of human CTLAA-CD59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTLA4; human; CD59; immune response inhibitor; xenotransplant rejection; transgenic; tissue donor; organ donor.
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Pred. No. 7.5e-07;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                   Score 96; DB 7; 1
Pred. No. 7.5e-07;
                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 2B2; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADL91002 standard; protein; 260 AA.
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ξ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI: 2003-766179/72.
                                                                                                                                                                                                        of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human CTLA4-CD59
                                                                                                                                                                                                                                                                  Sequence 260 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ADL91001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (FODO/) FODOR W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US2003157705-A1
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ADA50033 standard; protein; 261 AA.

ADA50033

(first entry)

20-NOV-2003

ADA50033;

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The sequence represents a CTLA4-CD59 chimeric protein, formed from porcine CTLA4 protein and human CD59 protein. Chimeric proteins comprising a domain having CSb-9 and/Or C3 inhibitory activity (e.g. CTLA4) and a domain having T-cell inhibitory activity (e.g. CD59) are capable of inhibiting both cellular immune responses and humoral immune responses. These polypeptides and their associated nucleic acids are useful for protecting pig cells of tissues and organs from both humoral and cellular rejection after xenotransplantation into humans. The sequences are capable of conferring resistance to humoral and cellular mechanisms of immune attack, to protect against human serum complement and to inhibit T-cell activation. Transgenic animals (for example, rodents, e.g. mouse, rat; lagomorphs, e.g. rabbit, hare; and ungulates, control protein animals (for example, rodents, e.g. pig, goat, sheep) expressing such a chimeric protein on the surfaces of their cells would have a higher chance of survival. (Updated on 11-SEP -2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric protein useful for protecting xenotransplanted tissues by inhibiting cellular both humoral and immune responses, comprises a C5b-9 and/or C3 inhibitory domain, and a T-cell inhibitory domain.
                                                                                                                                                                                                                                                                         CTLA4; CD59; human; pig; T-cell activation; C5b-9 inhibitory activity; C3 inhibitory activity; cellular immune response; xenotransplantation; humoral immune response; human serum complement; rodent; mouse; rabbit; rat; lagomorph; hare; ungulate; goat; sheep; mutant; mutein.
                                                                                                                                                                                                                                         Porcine CTLA4-human CD59 chimeric protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Fig 2A(2); 51pp; English.
                                                                                                            AAU00684 standard; protein; 261 AA
99US-0161186P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-OCT-2000; 2000WO-US029151
                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ALEX-) ALEXION PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fodor WL, Pizzolato M;
                                                                                                                                                                                    (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-300497/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAS00678.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-OCT-1999;
                                                                                                                                                                                    11-SEP-2003
07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                        sapiens
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                                                                                                                                                                                                                                                                                                                                                                                          scrofa.
                                                                                                                                              AAU00684;
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The invention relates to a chimaeric protein comprising a first domain capable of inhibiting a cellular immune response and a second domain capable of inhibiting a humoral immune response. Also included are a chimaeric DNA construct (comprising a DNA sequence encoding a domain capable of inhibiting a humoral immune response and a DNA sequence encoding a domain capable of inhibiting a humoral immune response), a condition a domain capable of inhibiting a humoral immune response), a cloning vector comprising the DNA construct, a host cell transformed by the vector, a transgenic cell, tissue, organ or mammal comprising the chimaeric protein, producing a mammal, mammalian organ, tissue or cells, where the mammal is useful as an organ donor for a human or organ, tissue or cells, where the protein defined above into the mammal, organ, tissue or cells, where the protein is expressed in the mammal, organ, tissue or cells, where the protein is expressed in the mammal, organ, tissue or cells, capions of the DNA appearing as ADA50036 which encodes the pig cTLA4 (cytotoxic T lymphocyte A4, also known as CDIS2) and defined regions of the portein ADA50037. The chimaeric protein is useful in the protection of the portein cell after xenotransplantation into a human, and in inhibiting humoral and cellular defence mechanism.

Chimaeras were produced comprising pig CTLA4 (cellular immune response region) and human CD59 (humoral response region), and of CTLA4 and human CD59 (contrarsor) and human CD59 chimaera
                                                                                                                                                                                     New chimeric proteins comprising a first domain and a second domain capabale of inhibiting a callular and humoral immune response, respectively, useful for regulating humoral and cellular effector functions of the immune system.
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WPI; 2003-625623/59.
                                                                N-PSDB; ADAS0032
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Gaps ö

Length 261; 0; Indels

100.0%; Score 96; DB 4; I 100.0%; Pred. No. 7.5e-07; Mismatches

. 0

Conservative

17;

Matches

Similarity

Query Match Best Local S

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RESULT 42

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Immunosuppressive, cellular immune response, humoral immune response, cytotoxic T lymphocyte A4; CD152; CTLA4; CD59; xenotransplantation, transplant rejection; human; pig.
                                                                                                       1. .25
/note= "Human CD59 leader peptide"
                                                                                                                                 /note= "Synthetic (Gly)6 linker"
159. .261
                                 Pig CTLA4/human CD59 chimaeric protein #1.
                                                                                                 Location/Qualifiers
                                                                                                                                               /note= "Human CD59"
                                                                                                                 26. .152
/note= "Pig CTLA4"
                                                                                                                                                                                                                                Fodor W;
                                                                                                                                                                                  20-AUG-2002; 2002US-00225519
                                                                                                                                                                                             10-AUG-2001; 2001US-00928267
                                                                                                                             .158
                                                                                                                                                                                                                                Costa C, Pizzolato M,
                                                                                                                                                                                                        COSTA C.
PIZZOLATO M.
                                                                                                                                                                                                                    FODOR W.
                                                                                                                                                          US2003086940-A1.
                                                                         Synthetic.
Homo sapiens.
                                                                                                                                                                      38-MAY-2003.
                                                                                      Sus scrofa.
                                                                    Chimeric
                                                                                                      Peptide
                                                                                                                  Protein
                                                                                                                                                                                                         (COST/)
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[mmunosuppressive; cellular immune response; humoral immune response;
                                                                                                                                     cytotoxic T lymphocyte A4; CD152; CTLA4; CD59; xenotransplantation; transplant rejection; human; pig.
                                                                                              Pig CTLA4/human CD59 chimaeric protein #3.
               ADA50056 standard; protein; 270 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                              20-AUG-2002; 2002US-00225519.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-AUG-2001; 2001US-00928267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (COST/) COSTA C.
(PIZZ/) PIZZOLATO M.
(FODO/) FODOR W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-625623/59.
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                                                                                                                                                                                                           Homo sapiens.
                                                                    20-NOV-2003
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                                                                                                                                                                                                                          Sus scrofa.
                                                                                                                                                                                              Synthetic.
                                         ADA50056;
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                                                                                                                                                                              Chimeric
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                                                                                                                                                                                                                                                                                                                                                  Protein
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  4DA50056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a chimeric protein capable of inhibiting both cellular and humoral immune responses. The protein and DNA molecules are useful in the prevention or treatment of humoral and cellular rejection of xenotransplants. In particular, the DNAs may be used to produce transpenic animals for use as tissue/organ donors, the cells of which are protected from human cellular immune responses due to their expression of
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the chimeric protein. The present sequence represents the amino acid sequence of a pig CTLA4-human CD59 chimeric protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New chimeric protein capable of inhibiting both cellular and humoral immune responses, and DNA constructs encoding the chimeric protein, useful for preventing and/or treating rejection of xenotransplants.
                                                                                                                                                                                                                                                                                                                  pig; CTLA4; human; CD59; immune response inhibitor; xenotransplant rejection; transgenic; tissue donor; organ donor.
                                                                                 ..
0
                                                      Length 261;
                                                                              0; Indels
                                                     100.0%; Score 96; DB 7; I
100.0%; Pred. No. 7.5e-07;
                                                                                 Mismatches
                                                                                                                                                                                                                                                                                          Pig CTLA4-human CD59 chimeric protein.
                                                                                                                                                                                                        ADL91000 standard; protein; 261 AA.
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                                                                                                                                   200 FEHCNFNDVTTRLRENE 216
                                                                                                             FEHCNFNDVTTRLRENE 17
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                                                                                                                                                                                                                                                               (first entry)
                                             Query Match
Best Local Similarity 100.7
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fodor WL, Pizzolato M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (FODO/) FODOR W L.
(PIZZ/) PIZZOLATO M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-766179/72.
N-PSDB; ADL90999.
of the invention.
                           Sequence 261 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 261 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                 JS2003157705-A1.
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                               20-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                             scrofa,
                                                                                                                                                                                                                                    ADL91000;
                                                                                                                                                                                                                                                                                                                                                                                         Chimeric.
                                                                                                                                                                                RESULT 43
                                                                                                                                                                                           ADL91000
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/note= "Synthetic (Asn-Ser)3 linker"

/note= "Pig CTLA4" 125. .130

.124

/note= "Human CD59"

131. .270

Fodor W;

Pizzolato M,

.. .37 'note= "Pig CTLA4 leader peptide"

Location/Qualifiers

(first entry)

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The invention relates to a chimaeric protein comprising a first domain capable of inhibiting a cellular immune response and a second domain capable of inhibiting a humoral immune response. Also included are a chimaeric DNA construct (comprising a DNA sequence encoding a domain capable of inhibiting a humoral immune response, a chimaeric DNA construct, a host cell transformed by the vector, a transgenic cell, tissue, organ or mammal comprising the chimaeric protein, producing a mammal, mammalian organ, tissue or cells, where the mammal is useful as an organ donor for a human or organ, tissue or cells, where the mammal is useful as an organ donor for a human or organ, tissue or cells, where the protein is expressed in the mammal, organ, tissue or cells, where the protein is expressed in the mammal, organ, tissue or cells, chimaeric protein is expressed in the mammal, organ, tissue or cells, defined regions of the DNA appearing as ADAS0036 which encodes the pig critA4 (cytocoxic I lymphocyte A4, also known as CDIS2) and defined cregions of the protein ADAS0037. The chimaeric protein is useful in the protection of the porcine cell after xenotransplantation into a human, and in inhibiting humoral and cellular defence mechanism.

Chimaeras were produced comprising pig CTLA4 (cellular immune response region) and human CDS9 (humoral response region), and of CTLA4 and human CDS9 chimaera
                                                                                                           New chimeric proteins comprising a first domain and a second domain capable of inhibiting a cellular and humoral immune response, respectively, useful for regulating humoral and cellular effector functions of the immune system.
                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 32-33; 59pp; English.
N-PSDB; ADAS0055
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Gaps

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0; Indels

100.0%; Score 96; DB 7; Length 261; 100.0%; Pred. No. 7.5e-07;

Mismatches

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17; Conservative

Best Local Similarity

Matches

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Query Match

FEHCNFNDVTTRLRENE 216

200

RESULT 44

1 FEHCNFNDVTTRLRENE 17

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sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      activity.
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Matches
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                                                                                                                                                                                                                                                                     Immunosuppressive; cellular immune response; humoral immune response; cytotoxic T lymphocyte A4; CD152; CTLA4; CD59; xenotransplantation; transplant rejection; human; pig.
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New chimeric proteins comprising a first domain and a second domain capable of inhibiting a cellular and humoral immune response, respectively, useful for regulating humoral and cellular effector functions of the immune system.
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                                            100.0%; Score 96; DB 7; Length 270; 100.0%; Pred. No. 7.8e-07; ive 0; Mismatches 0; Indels
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/note= "Pig CTLA4 leader peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                        Pig CTLA4/human CD59 chimaeric protein #4.
                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 35; 59pp; English.
                                                                                                                                                                           ADA50058 standard; protein; 271 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                 37. .125
/note= "Pig CTLA4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fodor W;
                                                                                                        209 FEHCNFNDVTTRLRENE 225
                                                                                          1 FEHCNFNDVTTRLRENE 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-AUG-2002; 2002US-00225519
                                                                                                                                                                                                                         (first entry)
                                                        Local Similarity 100.
Les 17; Conservative
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PIZZOLATO M.
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of the invention
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                       Sequence 270 AA;
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                                                                                                                                                                                                                                                                                                                                  Synthetic.
Homo sapiens.
Sus scrofa.
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                                              Query Match
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Matches
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the vector, a transgenic cell, tissue, organ or mammal comprising the chimaeric protein, producing a mammal, mammalian organ, tissue or cells, where the mammal is useful as an organ donor for a human or organ, tissue or cells, or cells transplant into a human, by inserting a nucleic acid encoding a chimaeric protein defined above into the mammal, organ, tissue or cells, where the protein is expressed in the mammal, organ, tissue or cells, defined regions of the DNA appearing as ADAS0036 which encodes the pig regions of the CTLA4 (cycloxic T lymphocyte A4, also known as CD152) and defined regions of the CTLA4 protein ADAS0037. The chimaeric protein is useful in the protection of the porcine cell after xenotransplantation into a human, and in inhibiting humoral and cellular defence mechanism. Chimaeras were produced comprising pig CTLA4 (cellular immune response region) and human CD59 (humoral response region), and of CTLA4 and human DAP (not defined). The present sequence represents a CTLA4/CD59 chimaera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; CDS9; complement inhibitor; gene; ds; complement receptor 2; CR2; chimeric; immunoconjugate; cancer; Hodgkin's lymphoma; myeloid leukaemia; hypoxic tumour; viral infection; inflammatory condition; rheumatoid arthritis; Crohn's disease; systemic lupus erythematosus;
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100.0%; Pred. No. 7.8e-07;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADO41954 standard; protein; 330 AA
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activity. Specifically, it refers to immunoconjugate compositions comprising a construct that has a complement inhibitor linked to the CR2, which can be used modulate the complement system i.e. the series of blood proteins that are major effectors of the immune system. The present invention describes compositions that can be used to treat various cancers including Hodgkin lymphoma, myeloid leukaemia and hypoxic tumours, viral infections such as herpes simplex virus, cytomegalovirus and Epstein-Barr virus, as well as inflammatory conditions for example Accordingly, these compositions exhibit cytostatic, antiathematosus. Accordingly, these compositions exhibit cytostatic, antiathematic, antiinflammatory, dermatological, immunosuppressive, antiathritic, antiinflammatory dermatological, immunosuppressive, antiathritic, antiinflammatory adraticities. This polypeptide sequence is the human CDS9-CR2 fusion protein (CDS9 is a complement inhibitor) of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human; CD59; complement inhibitor; gene; ds; complement receptor 2; CR2; chimeric; immunoconjugate; cancer; Hodgkin's lymphoma; myeloid leukaemia; hypoxic tumour; viral infection; inflammatory condition; relumnatory condition; rheumatoid arthritis; Crohn's disease; systemic lupus erythematosus; cytostatic; antiaristhmatic; antianflammatory; dermatological; immunosuppressive; antiarthritic; antirheumatic; vasotropic; antidiabetic; neuroprotective; antiallergic; antiulcer; antiviral;
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                                                                                                                                                                                                                                                                                                                     100.0%; Score 96; DB 8; Length 330; 100.0%; Pred. No. 9.6e-07;
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Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                       Query Match
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activity. Specifically, it refers to immunoconjugate compositions comprising a construct that has a complement inhibitor linked to the CR2, which can be used modulate the complement system i.e. the series of blood proteins that are major effectors of the immune system. The present
                                                                                            invention describes compositions that can be used to treat various cancers including Hodgkin lymphoma, myeloid leuksemia and hypoxic tumours, viral infections such as herpes simplex virus, cytomegalovirus and Epstein-Barr virus, as well as inflammatory conditions for example Accordingly, these compositions exhibit cytostatic, antiasthmatics antiinflammatory, dermatological, immunosuppressive, antiarthmitic, antiinflammatic, vasotropic, antidiabetic, neuroprotective, antiallergic, antiulcer and antiviral activities This polypeptide sequence is the human CR2-CD59 fusion protein (CD59 is a complement inhibitor) of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 9.8e-07;
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Best Local Similarity 100.0
----hes 17; Conservative
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N-PSDB; ADO41949.
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41, Appl 9, Appli 8, Appli 6, Appli 7, Appli 12, Appli 25, Appli 26, Appli 26, Appli 10, Appli

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Perfect score:

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Sequence:

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Sequence 41, Ar
Sequence 37475,
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Sequence 2
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Publication No. US20050032128A1
GENERAL INFORMATION:
APPLICANT HAlperin, Jose
TITLE OF INVENTION: ANT-GLYCATED CD59 ANTIBODIES AND USES THEREOF
FILE REFERENCE: H0498.70223US00
CURRENT APPLICATION NUMBER: US/10/870,342A
CURRENT FILING DATE: 2004-06-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                               Sequence
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; Sequence 20, Application US/10870342A
; PADILication No. US20050032128A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
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US-10-332-047-4
US-10-332-047-4
US-10-322-047-5
US-10-332-047-9
US-10-332-047-9
US-10-332-047-9
US-10-332-047-9
US-10-332-047-9
US-10-332-047-9
US-10-332-047-9
US-10-332-047-9
US-10-870-342A-6
US-10-870-342A-7
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US-10-928-267-25
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US-10-928-267-13
US-10-928-267-13
US-10-928-267-13
US-10-928-267-13
US-10-928-267-13
US-10-225-519-25
US-10-870-342A-13
US-10-870-342A-13
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 ORGANISM: Homo sapiens
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Best Local Similarity
Matches 17; Conserv
 US-10-870-342A-14
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TYPE: PRT
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Sequence 15, Appl
Sequence 18, Appl
Sequence 3, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
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                                                                                                  8, 2005, 11:40:17; Search time 154 Seconds (without alignments) 42.316 Million cell updates/sec
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Sequence 1, Ag
Sequence 37, 7
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB_pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB_pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
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7: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
21: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
22: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                         1710399
                GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-10-870-342A-15
US-10-870-342A-15
US-10-870-342A-18
US-10-332-047-3
US-10-742-887-42
US-10-742-887-42
US-10-742-877-45
US-10-332-047-6
US-10-742-887-17
US-10-742-887-17
                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                              1710399 segs, 383334425 residues
                                                                                                                                                                                                                                                                                                                                                                                           Listing first 45 summaries
                                                                        OM protein - protein search, using sw model
                                                                                                                                                   US-09-020-393B-3_COPY_42_58
96
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Maximum DB seq length: 2000000000
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286
330
70
71
77
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Match
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No. Result

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1 FEHCNFNDVTTRLRENE 17
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US-10-742-887-39
                         RESULT 5
JS-10-332-047-3
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                                                                                                                                                                                                                                                                                                                                                       Sequence 15, Application US/10870342A
Publication No. US20050032128A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
FILE REFERENCE: H0498.70223US00
CURRENT FILING DAIR: 2004-06-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin version 3.2
LENGTH: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18, Application US/10870342A
Publication No. US20050032128A1
GENERAL INFORMATION:
APPLICANT: Halperin, Jose
TITLE OF INVENTICH: HO498.70223US00
CURRENT FILING DATE: 2004-06-17
NUMBER OF SEQ ID NOS: 49
SSQ ID NO 18
LENGTH: 42
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                                                                                                                                                                                      Length 26;
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100.0%; Pred. No. 3.9e-08;
iive 0; Mismatches 0;
                                                                                                                                                                                    100.0%; Score 96; DB 17; 100.0%; Pred. No. 2.3e-08;
                                                                                                                                                                                                                    0; Mismatches
FILE REFERENCE: H0498.70223US00
CURRENT APPLICATION NUMBER: US/10/870,342A
CURRENT FILING DATE: 2004-06-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn version 3.2
SEQ ID NO 20
LENGTH: 26
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                                                                                                                                                                                                                   17; Conservative
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Matches 17; Conservative
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                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 17; Conserv
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Best Local Similarity
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US-10-870-342A-15
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US-10-870-342A-18
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein APT634
US-10-742-887-39
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| Sequence 39, Application US/10742887
| Publication No. US20040266684A1
| GENERAL INFORMATION:
| APPLICANT: MOSSAKOWSKA, DANUTA EWA IRENA
| APPLICANT: MOSSAKOWSKA, DANUTA EWA IRENA
| TITLE OF INVENTION: CONUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH
| TITLE OF INVENTION: CONUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH
| TITLE OF INVENTION: CONUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH
| TITLE OF INVENTION: CONUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH
| TITLE OF INVENTION: CONUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH
| FILE REFERENCE: 37945-004
| CURRENT PAPLICATION NUMBER: US/09/612,314
| PRIOR APPLICATION NUMBER: US/09/612,314
| PRIOR FILING DATE: 1999-03-16
| PRIOR FILING DATE: 1999-03-16
| PRIOR FILING DATE: 1999-07-08
| PRIOR FILING DATE: 1996-07-15
| NUMBER OF SEQ ID NOS: 53
| SEQ ID NO 39
| LENGTH: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
Sequence 3, Application US/10332047
; Bequence 3, Application US/10332047
; Publication No. US20040043432A1
; GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: ROWLING, PAMELA JANE ELIZABETH
APPLICANT: RITLEY, SIMON HUGH
TITLE OF INVENTION: COMPOUNDS TARGETED TO CELLULAR LOCATIONS
FILE REFERENCE: 37945-0044
; CURRENT APPLICATION NUMBER: US/10/332,047
; CURRENT FILING DATE: 2001-0-06
; PRIOR APPLICATION NUMBER: PCT/GB01/03034
; PRIOR APPLICATION NUMBER: PCT/GB01/03034
; PRIOR PLIING DATE: 2001-0-06
; PRIOR PLIING DATE: 2001-0-07
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 3
; LENGTH: 70
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100.0%; Score 96; DB 15;
Best Local Similarity 100.0%; Pred. No. 6.8e-08;
Matches 17; Conservative 0; Mismatches 0;
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100.0%; Score 96; DB 16;
Best Local Similarity 100.0%; Pred. No. 6.8e-08;
Matches 17; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
FEATURE:
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Gaps

8

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Sequence 3, Application US/10403340
Publication No. US20030166565A1
GENERAL INPORMATION:
APPLICANT: Sims, Peter J.
TITLE OF INVENTION: Compositions and Methods to Inhibit the C5b-9 Complex of Complement
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                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 W. Peachtree St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 77;
        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
COMPUTER: IBM PC TOMBY STATES
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/403,340
FILING DATE: 77-Mar-2003
CLASSIFICATION: 514
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Local Similarity 100.0%; Score 96; DB 14;
Local Similarity 100.0%; Pred. No. 7.5e-08;
Nes 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/020,393B
FILING DATE: 03-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Paber, Patrea L.
REGISTRATION NUMBER: 31,284
REFIERENCE/DOCKET NUMBER: OMRF 170
     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Human
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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APPLICANT: SMITH, GEOFFREY PAUL
APPLICANT: RIDLEY, SIMON HUGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION
TELEPHONE: 404-873-8794
TELEFAX: 404-873-8795
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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                                                        1 FEHCNFNDVTTRLRENE 17
                                                                                     42 FEHCNFNDVTTRLRENE 58
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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     17;
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     Matches
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US-10-742-887-42
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US-10-332-047-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOLUBLE PEPTIDIC COMPOUNDS WITH
                                                                                                                                             | Sequence 6, Application US/10332047 |
| Publication No. US20040043432A1 |
| CENERAL INFORMATION: |
| APPLICANT: SMITH, GEOFFREY PAUL |
| APPLICANT: SMITH, GEOFFREY PAUL |
| APPLICANT: RIDLEY, SIMON HUGH |
| TITLE OF INVENTION: COMPOUNDS TARGETED TO CELLULAR LOCATIONS |
| FILE REFERENCE: 37945-0044 |
| CURRENT APPLICATION NUMBER: US/10/332,047 |
| CURRENT APPLICATION NUMBER: PCT/GB01/03034 |
| PRIOR FILING DATE: 2001-07-06 |
| PRIOR FILING DATE: 2000-07-07 |
| NUMBER OF SEQ ID NOS: 15 |
| SOFTWARE: Patentin Ver. 2.1
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Pred. No. 6.9e-08;
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(NS-10.742-887-42)

(Sequence 42, Application US/10742887)

(PUBLICALIN NO. US20004026684A1)

(GENERAL INFORMATION:

APPLICANT: SMITH, RICHARD ANTHONY GODWIN

APPLICANT: DODD, IAN

TITLE OF INVENTION: CONJUGATES OF SOLUBLE PEPTIIC

TITLE OF INVENTION: MEMBRANE-BINDING AGENTS

FILE REFERENCE: 37945-0004

CURRENT APPLICATION NUMBER: US/10/742,887

CURRENT APPLICATION NUMBER: US/09/612,314

PRIOR PILING DATE: 2003-12-23

PRIOR FILING DATE: 1990-03-16

PRIOR APPLICATION NUMBER: US/09/612,314

PRIOR FILING DATE: 1990-03-16

PRIOR APPLICATION NUMBER: US/09/612,314

PRIOR APPLICATION NUMBER: US/09/612,314

PRIOR PRILING DATE: 1990-03-16

PRIOR APPLICATION NUMBER: US/09/612,314

PRIOR APPLICATION UMBER: US/09/612,314
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100.0%;
FEHCNFNDVTTRLRENE 58
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
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Best Local Similarity
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LENGTH: 71
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LENGTH: 71
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Gaps

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US-10-742-887-40
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US-10-332-047-5
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GENERAL INFORMATION:
APPLICANT: SMITH, RICHARD ANTHONY GODWIN
APPLICANT: BODD, IAN
APPLICANT: BODD, IAN
APPLICANT: CONJUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH
ITILE OF INVENTION: MEMBRANE-BINDING AGENTS
ITILE OF INVENTION: MEMBRANE-BINDING AGENTS
FILE REPRESENTS: 2003-12-23
FRICE APPLICATION NUMBER: US/09/612,314
PRIOR APPLICATION NUMBER: US/09/612,314
PRIOR PRILING DATE: 2003-12-03-16
PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1999-03-16
PRIOR PRILING DATE: 1999-03-16
PRIOR PRILING DATE: 1999-03-16
PRIOR PRILING DATE: 1999-03-16
PRIOR PRILING DATE: 1996-07-15
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PARLENTIN VET: 2.1
SEQ ID NOS: 53
LENGTH: 77
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; TITLE OF INVENTION: COMPOUNDS TARGETED TO CELLULAR LOCATIONS; FILE REFERENCE: 37945-0044
; CURRENT APPLICATION NUMBER: US/10/332,047
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: PCT/GB01/03034
; PRIOR APPLICATION NUMBER: GB 0016811.2
; PRIOR APPLICATION NUMBER: GB 0016811.2
; RIOR PILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.1
; LENGTH: 77
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Best Local Similarity 100.0%; Pred. No. 7.5e-08; Matches 17; Conservative 0; Mismatches 0;
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Publication No. US20040043432A1
GENERAL INFORMATION:
APPLICANT: ROWLING, PAMELA JANE ELIZABETH
APPLICANT: SMITH, GEOFFREY PAUL
APPLICANT: RIDLEY, SIMON HUGH
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ORGANISM: Artificial Sequence
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ORGANISM: Homo sapiens
US-10-332-047-1
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US-10-742-887-37
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US-10-332-047-4
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein APT2060
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APPLICANT: SMITH, RICHARD ANTHONY GODWIN

APPLICANT: DODD, IAN

APPLICANT: DODD, IAN

APPLICANT: MOSSAKOWSKA, DANUTA EWA IRENA

ITILE OF INVENTION: WEMBRANE-BINDING AGENTS

ITILE OF INVENTION: WEMBRANE-BINDING AGENTS

ITILE OF INVENTION: WEMBRANE-BINDING AGENTS

ITILE OF INVENTION: WOMBREN: US/10/742,887

CURRENT APPLICATION NUMBER: US/99/612,314

PRIOR APPLICATION NUMBER: US/99/612,314

PRIOR APPLICATION NUMBER: US/99/14,913

PRIOR PELLING DATE: 1999-03-16

PRIOR APPLICATION NUMBER: US/T/EP97/03715

PRIOR APPLICATION NUMBER: GB 96 148 71.3

PRIOR PELLING DATE: 1996-07-15

NUMBER OF SEQ ID NOS: 53

SEQ ID NO 40

IENGTH: 82
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; TITLE OF INVENTION: COMPOUNDS TARGETED TO CELLULAR LOCATIONS
; CURRENT APPLICATION NUMBER: US/10/332,047
; CURRENT PELING DATE: 2003-01-06
; PRIOR PAPLICATION NUMBER: PCT/GB01/03034
; PRIOR APPLICATION NUMBER: PCT/GB01/03034
; PRIOR PELING DATE: 2001-07-06
; PRIOR PELING DATE: 2001-07-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PARCHIN Ver. 2.1
; SEQ ID NO 4
; LENGTH: 82
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Publication No. US20040266684A1
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 17; Conservative
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Best Local Similarity 100.0
Matches 17; Conservative
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
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Sequence 9, Application US/10332047
Publication No. US20040043432A1
GENERAL INFORMATION:
APPLICANT: ROWLING:
APPLICANT: ROMING, GEOFPREY PAUL
APPLICANT: RIDLEY, SIMON HUGH
TITLE OF INVENTION: COMPOUNDS TARGETED TO CELLULAR LOCATIONS
FILE REFERENCE: 37945-0044
CURRENT FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: PCT/GB01/03034
PRIOR FILING DATE: 2001-07-06
PRIOR FILING DATE: 2001-07-06
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 9
LENGTH: 88
LENGTH: 88
LENGTH: 88
LENGTH: 88
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Sequence 7. Application US/10332047

Publication No. US2004004332A1

GENERAL INFORMATION:

APPLICANT: ROWLING.

APPLICANT: ROWLING.

APPLICANT: RITH, GEOFFREY PAUL

APPLICANT: RITH, GEOFFREY PAUL

APPLICANT: RIDLEY, SIMON HUGH

TITLE OF INVENTION: COMPOUNDS TARGETED TO CELLULAR LOCATIONS

FILE REFERENCE: 37945-0044

CURRENT PILING DATE: 2003-01-06

PRIOR APPLICATION NUMBER: PCT/GB01/03034

PRIOR APPLICATION NUMBER: PCT/GB01/03034

PRIOR APPLICATION NUMBER: GB 0016811.2

PRIOR APPLICATION NUMBER: GB 0016811.2

PRIOR APPLICATION NUMBER: GB 0016811.2

SEQ ID NO 7

SEQ ID NO 7

LENGTH: 99
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US-10-332-047-8
; Sequence 8, Application US/10332047
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ORGANISM: Artificial Sequence
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Matches 17; Conserv
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US-10-332-047-7
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US-10-742-887-41
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APPLICANT: BODD, IAN
APPLICANT: DODD, IAN
APPLICANT: DODD, IAN
TITLE OF INVENTION: CONJUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH
TITLE OP INVENTION: MEMBRANE-BINDING AGENTS
FILE REPREMENCE: 37945-0004
CURRENT APPLICATION NUMBER: US/10/742,887
CURRENT PILING DATE: 2003-12-23
PRIOR APPLICATION NUMBER: US/09/612,314
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1999-03-16
PRIOR PILING DATE: 1999-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: peptide
US-10-332-047-5
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     APPLICANT: ROWLING, PAMELA JANE ELIZABETH
APPLICANT: SMITH, GEOFFREY PAUL
TITLE OF INVENTION: COMPOUNDS TARGETED TO CELLULAR LOCATIONS
FILE REFERENCE: 37945-0044
CURRENT APPLICATION NUMBER: US/10/332,047
CURRENT FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: PCT/GB01/03034
PRIOR APPLICATION NUMBER: PCT/GB01/03034
PRIOR APPLICATION NUMBER: GB 0016811.2
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTING VET: 2.1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 83;
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100.0%; Score 96; DB 15;
Best Local Similarity 100.0%; Pred. No. 8.1e-08;
Matches 17; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 41, Application US/10742887; Publication No. US20040266684A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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US-10-742-887-41
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US-10-332-047-9
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LENGTH: 83
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US-10-870-342A-7
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    LENGTH: 103
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Publication No. US20050032128A1
GENERAL INFORMATION:
APPLICANT: HALDERIN, JOSE
TITLE OF INVENTION: ANTI-GLYCATED CDS9 ANTIBODIES AND USES THEREOF
FILE REFERENCE: H0498, 70223US00
CURRENT APPLICATION NUMBER: US/10/870,342A
CURRENT FILING DATE: 2004-06-17
NUMBER OF SEQ ID NOS: 49
SOFWARE: Patentin version 3.2
SEQ ID NO 7
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Publication No. US20050032128A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTON: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
TITLE OF INVENTON: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/870,342A
CURRENT FILING DATE: 2004-06-17
UNMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: peptide US-10-332-047-8
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                                     APPLICANT: ROWLING, PAMELA JANE ELIZABETH
APPLICANT: SMITH, GEOFREY PAUL
APPLICANT: SMITH, GEOFREY PAUL
APPLICANT: RIDLEY, SIMON HUGH
TITLE OF INVENTION: COMPOUNDS TARGETED TO CELLULAR LOCATIONS
TILLE REFERENCE: 37945-0044
CURRENT APPLICATION NUMBER: US/10/332,047
CURRENT FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: PCT/GB01/03034
PRIOR APPLICATION NUMBER: GB 0016811.2
PRIOR FILING DATE: 2000-07-06
PRIOR APPLICATION NUMBER: GB 0016811.2
PRIOR FILING DATE: 2000-07-07
NUMBER: OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
SEQ ID NOS: 15
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Publication No. US20040043432A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
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Best Local Similarity 100.
Matches 17; Conservative
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LENGTH: 103
TYPE: PRT
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US-10-870-342A-7
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US-10-870-342A-6
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APPLICANT: Messier, Walter
TITLE OF INVENTION: Methods to Identify Polynucleotide and Polypeptide Sequences
TITLE OF INVENTION: Which may be Associated with Physiological and Medical Conditions
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APPLICANT: Halperin, Jose
TITLE OF INVENTION:
ANTI-GINCATED CD59 ANTIBODIES AND USES THEREOF
FILE REPERENCE: HQ498.702230850
CURRENT APPLICATION NUMBER: US/10/870,342A
CURRENT FILING DATE: 2004-06-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin version 3.2
SEQ ID NO 8
LENGTH: 103
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Best Local Similarity 100.0%; Pred. No. 1e-
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NAME/KEY: misc feature
LOCATION: (65)...(66)
OTHER INPORMATION: Lys is glycated
FEATURE:
NAME/KEY: misc_feature
LOCATION: (85)...(85)
OTHER INFORMATION: Lys is glycated
TYPE: PRT
ORGANISM: Homo sapiens
FRATURE:
UNAME/KEY: misc_feature
LOCATION: (41)..(41)
OTHER INFORMATION: Lys is glycated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: misc_feature
NAME/KEY: misc_feature
CATION: (14)..(14)
OTHER INFORMATION: Lys is glycated
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/10870342A Publication No. US20050032128A1
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; Sequence 12, Application US/10883576
; Publication No. US20050037400A1
; GENERAL INFORMATION:
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OTHER INFORMATION: Lys is glycated
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Best Local Similarity 100.
Matches 17; Conservative
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NAME/KEY: misc feature
LOCATION: (30)...(30)
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LOCATION: (41)..(41)
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NS-09-928-267-25

| Sequence 25, Application US/09928267
| Sequence 25, Application US/09928267
| Publication No. US20030157705A1
| GENERAL INFORMATION:
| APPLICANT: William, Fodox
| TITLE OF INVENTION: BUGINEERED RECOMBINANT MOLECULE THAT REGULATES HUMORAL AND |
| TITLE OF INVENTION: CELLULAR EFFECTOR FUNCTIONS OF THE IMMUNE SYSTEM |
| FILE REFERENCE: 1087-19 |
| CURRENT APPLICANTON NUMBER: US/09/928,267 |
| CURRENT PILING DATE: 2011-08-10 |
| NUMBER OF SEQ ID NOS: 27 |
| SOFTWARE: Patentin version 3.2 |
| LENGTH: 128 |
| TYPE: PRT |
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Publication No. US20030157705A1

GENERAL INFORMATION:

TITLE OF INVENTION: CELLULAR EFFECTOR FUNCTIONS OF THE IMMUNE SYSTEM
TITLE OF INVENTION: CELLULAR EFFECTOR FUNCTIONS OF THE IMMUNE SYSTEM
CURRENT APPLICATION NUMBER: US/09/928,267

CURRENT PILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin version 3.2

SEQ ID NO 26

LENGTH: 128
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                                                                                                                                                                                                                                                                                                                                                                            Length 127;
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Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.3e-07;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                     ORGANISM: Human
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                              LENGTH: 127 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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                        SEQUENCE CHARACTERISTICS:
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Matches 17; Conservative
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Best Local Similarity
Matches 17; Conserv
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US-09-928-267-25
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ORGANISM: human
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Publication No. US20030166565A1
GENERAL INFORMATION:
APPLICANT: Sims, Peter J.
TITLE OF INVENTION: Compositions and Methods to Inhibit the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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CORRESPONDENCE ADDRESS:
ADDRESSE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 W. Peachtree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 105;
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STATE: GA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: PATENTY PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/10/403,340
FILING DATE: 27-Mar-2003
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Pred. No. 1.1e-07;
; Mismatches 0;
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APPLICATION NUMBER: US/09/020,393B
FILING DATE: 03-FEB-1998
ATTORNEY/AGENT INFORMATION:
FILE REFERENCE: GENO200.2 CIP3
CURRENT APPLICATION NUMBER: US/10/883,576
CURRENT FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: US 10/098,600
PRIOR PILING DATE: 2002-03-14
PRIOR PILING DATE: 2002-03-14
PRIOR FILING DATE: 2004-06-30
PRIOR PILING DATE: 2003-06-30
PRIOR PILING DATE: 2000-06-09
PRIOR PILING DATE: 2000-06-09
PRIOR PILING DATE: 1999-01-29
PRIOR PILING DATE: 1999-01-29
PRIOR PILING DATE: 1998-09-02
PRIOR PILING DATE: 1998-09-03
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REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF 170
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TELEPHONE: 404-873-8794
INFORMATION FOR SEQ ID NO: 1:
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Best Local Similarity 100.0%;
Matches 17; Conservative 0
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US-10-403-340-1
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Publication No. US20050032128A1
GENERAL INFORMATION.
APPLICANT: Halperin, Jose
TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
FILE REPERENCE: HO498.7022300500
CURRENT APPLICATION NUMBER: US/10/870,342A
CURRENT FILING DATE: 2004-06-17
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                                                               APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Saven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale B.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT PRILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077-04-04
SEQ ID NO: 3077-04-04
SEQ ID NO: 118
LENGTH: 128
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100.0%; Score 96; DB 16; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels
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; Sequence 20, Application US/10759181A
; Publication No. US20040163140A1
; GENERAL INFORMATION:
    APPLICANT: MORGAN, BRYAN P.
; APPLICANT: RUSHWERE, NEIL K.
; APPLICANT: HINCHLIFFE, STEWART J.
APPLICANT: HINCHLIFFE, STEWART J.
TITLE OF INVENTION: MODIFIED BIOLOGICAL MATERIAL
FILE REFERENCE: WN/KH/JJ/WCM
CURRENT FILLING DATE: 1299-04-08
; PRIOR APPLICATION NUMBER: PCT/GB99/01085
; PRIOR FILLING DATE: 1999-04-08
; PRIOR PILLING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO S. CARLOWS CONTRACTOR CONTRIBUTION NUMBER: PATOMER CONTRIBUTION NUMBER: CB SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO S. CARLOWS CONTRIBUTION NUMBER: PATOMER CARLOWS CONTRIBUTION NUMBER: CB SEQ ID NOS: 24
; SOFTWARE: PATENTH: 128
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   Ghosh, Soumitra S.
Fahy, Eoin D.
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Best Local Similarity 100.0
Matches 17; Conservative
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ORGANISM: Homo sapiens
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US-10-759-181A-20
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US-10-207-655-109
Sequence 109, Application US/10207655
Publication No. US20030118592A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.;
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069, 401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
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US-10-408-765A-1118
Sequence 1118, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
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67 FEHCNFNDVTTRLRENE 83
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Best Local Similarity 100.0
Matches 17; Conservative
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Best Local Similarity 100.
Matches 17; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
US-10-207-655-109
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) ORGANISM: Homo sapiens
US-10-128-558-132
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Best Local Similarity
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ORGANISM: human
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100.0%; Score 96; DB 17;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                          Query Match
100.0%; Score 96; DB 17;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0;
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| Sequence 132, Application US/1012858
| Publication No. US20040219521A1
| GENERAL INFORMATION:
| APPLICANT: Wang, Zhiwei
| APPLICANT: Wang, Zhiwei
| APPLICANT: Weng, Cazhi
| APPLICANT: Weng, Cazhi
| APPLICANT: Drmanac, Radoie T
| TITLE OF INVENTION: Polypeptides
| FILE REFERENCE: B12AA
| CURRENT APPLICATION NUMBER: US/10/128,558
| CURRENT FILING DATE: 2002-04-22
| PRIOR APPLICATION NUMBER: US 09/488,725
| PRIOR FILING DATE: 2000-01-21
| PRIOR PILING DATE: 2000-01-21
| PRIOR FILING DATE: 2000-01-21
| PRIOR FILING DATE: 2000-01-25
| PRIOR PILING DATE: 2000-01-25
| PRIOR FILING DATE: 2000-01-25
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TITLE OF INVENTION: OnCOLOGY drug innovation
TITLE REFERENCE: P 573 PC00
CURRENT APPLICATION NUMBER: US/10/482,029
CURRENT FILING DATE: 2003-12-29
SUPMER OF SEQ ID NOS: 437
SOFTWARE: PatentIn version 3.1
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Publication No. US20050037445A1
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin version 3.2
SEQ ID NO 5
LENGTH: 128
                                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-342A-5
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US-10-482-029-98
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LENGTH: 128
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Sequence 13, Application US/09928267

Sequence 13, Application US/09928267

Publication No. US20030157705A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: CELLULAR EFFECTOR FUNCTIONS OF THE IMMUNE SYSTEM

TITLE OF INVENTION: CELLULAR EFFECTOR FUNCTIONS OF THE IMMUNE SYSTEM

TITLE OF INVENTION: US/09/928,267

CURRENT APPLICATION NUMBER: US/09/928,267

CURRENT FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin version 3.2

SEQ ID NO 13

LENGTH: 260

TYPE: PRT
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Sequence 14, Application US/09928267

Sequence 14, Application US/09928267

Publication No. US20030157705A1

GENERAL INFORMATION:

TITLE OF INVENTION: ENGINEERED RECOMBINANT MOLECULE THAT REGULATES HUMORAL AND TITLE OF INVENTION: ENGINEERED REFECTOR FUNCTIONS OF THE IMMUNE SYSTEM FILE REFERENCE: 108-19

CURRENT PELICA DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 27

SOFTWARE PATENCE: PATENCE: 201-08-10

SOFTWARE PATENCE: PATENCE: 201-08-10
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PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR PAPLICATION NUMBER: PCT/USO1/03800
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2000-02-05
PRIOR PILICATION NUMBER: US 09/515,126
PRIOR APPLICATION AUMBER: US 09/515,126
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 412
SOFTWARE: PL FL genes Version 6.0
LENGTH: 190
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Pred. No. 2.8e-07;
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100.0%; Score 96; DB
Best Local Similarity 100.0%; Pred. No. 2.8
Matches 17; Conservative 0; Mismatches
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Sequence 2, Application US/10225519

Sequence 2, Application US/10225519

Sequence 2, Application No. US2030086940A1

GENERAL INFORMATION:

APPLICANT: Costa, Cristina

APPLICANT: Costa, Cristina

TITLE OF INVENTION: BFFECTOR FUNCTIONS OF THE IMMUNE SYSTEM

TITLE OF INVENTION: BFFECTOR FUNCTIONS OF THE IMMUNE SYSTEM

FILE REFERENCE: 33-CIP

CURRENT FILING DATE: 2002-08-20

FRIOR APPLICATION NUMBER: US/10/225,519

FRIOR PILING DATE: 2001-08-10

FRIOR APPLICATION NUMBER: PCT/US00/29151

FRIOR PILING DATE: 1999-10-22

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin version 3.1

SEQ ID NO 2

LENGTH: 261

LENGTH: 261
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OTHER INFORMATION: DNA used in the cloning of porcine CTLA4 - human CD59 chimeric mo OTHER INFORMATION: lecules.
NAME/KEY: misc feature
LOCATION: (38)...(112)
OTHER INFORMATION: CD59 leader peptide region
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/09928267
Sequence 10, Application US/09928267
GENERAL INFORMATION:
TITLE OF INVENTION: ENGINEERED RECOMBINANT MOLECULE THAT REGULATES HUMORAL AND TITLE OF INVENTION: CELLULAR EFFECTOR FUNCTIONS OF THE IMMUNE SYSTEM FILE REFERENCE: 1097-19
CURRENT APPLICATION NUMBER: US/09/928,267
CURRENT FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 10
LENGTH: 261
TYPE: PAT
TYPE: PAT
ORGANISM: pig and human
US-09-928-267-10
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tches 0;
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100.0%; Pred. No. 2.8e-07;
iive 0; Mismatches 0;
                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 17; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
                           ; ORGANISM: pig and human US-09-928-267-9
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US-09-928-267-10
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                                                                                                                                                                                                    Sequence 4, Application US/1025519

Publication No. US2003008694041

GENERAL INFORMATION:

APPLICANT: Costa, Cristina

APPLICANT: Fodor, William L.

TITLE OF INVENTION: AN EFFECTOR FUNCTIONS OF THE IMMUNE SYSTEM

FILE REFRENCE: 33-CIP

CURRENT APPLICATION NUMBER: US/10/225,519

CURRENT APPLICATION NUMBER: US 09/928,267

PRIOR APPLICATION NUMBER: US 09/928,267

PRIOR PILING DATE: 2000-08-10

PRIOR FILING DATE: 2000-08-10

PRIOR FILING DATE: 2001-021

PRIOR FILING DATE: 2000-10-21

PRIOR FILING DATE: 2000-10-22

NUMBER OF SEQ ID NOS: 27

SEOFTWARE PRICHT NOS: 27

SOFTWARE PATENTING DATE: 27

NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PERTURE:
OTHER INFORMATION: DNA used in the cloning of human CTLA4 - human CD59 chimeric mole OTHER INFORMATION: cules.
NAME/KEY: misc feature
LOCATION: (37) ... (111)
OTHER INFORMATION: CD59 leader peptide region
NAME/KEY: misc feature
LOCATION: (118) ... (489)
OTHER INFORMATION: CTLA4 coding region
NAME/KEY: misc feature
LOCATION: (490) ... (507)
OTHER INFORMATION: (AS)3 linker region.
NAME/KEY: misc feature
LOCATION: (508) ... (816)
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Sequence 9, Application US/09928267

Publication No. US20030157705A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ENGINEERED RECOMBINANT MOLECULE THAT REGULATES HUMORAL AND TITLE OF INVENTION: CELLULAR EFFECTOR FUNCTIONS OF THE IMMUNE SYSTEM TITLE OF INVENTION: US/09/928, 267

CURRENT APPLICATION UNDER: US/09/928, 267

CURRENT FILING DATE: 2001-08-10

SOFTWARE PATENTING DATE: 2001-08-10

SOFTWARE PATENTING PATE: 2001-08-10

SUMMARR OF SEQ ID NOS: 27

SEQ ID NO 9

LENGTH: 261
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0; Indels
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                                                                                            199 FEHCNFNDVTTRLRENE 215
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ORGANISM: Artificial Sequence
17; Conservative
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Matches 17; Conservative
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LENGTH: 260
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Matches
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APPLICANT: Costa, Cristina
APPLICANT: Pizzolato, Maryellen C.
APPLICANT: Pizzolato, Maryellen C.
APPLICANT: Pizzolato, Maryellen C.
APPLICANT: Podor, William L.
ITILE OF INVENTION: AN ENGINEERE RECOMBINANT MOLECULE THAT REGULATES HUMORAL AND CELI;
ITILE OF INVENTION: EFFECTOR FUNCTIONS OF THE IMMUNE SYSTEM
FILE REPERENCE: 33-C1P
CURRENT APPLICATION NUMBER: US 09/225,519
CURRENT FILING DATE: 2002-08-20
FRIOR FILING DATE: 2000-10-21
FRIOR APPLICATION NUMBER: PCT/US00/29151
FRIOR APPLICATION NUMBER: US 60/161,186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Chimeric porcine CTLA4-human CD59 with porcine CTLA4 leader seque OTHER INFORMATION: nce and (G)6 linker region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (24)...(134)
OTHER INFORMATION: Porcine CTLA4 leader sequence.
NAME/KEY: misc feature
LOCATION: (135)...(509)
OTHER INFORMATION: Porcine CTLA4 coding sequence.
NAME/KEY: misc feature
LOCATION: (510)...(527)
OTHER INFORMATION: (6) finker region.
NAME/KEY: misc feature
LOCATION: (520)...(836)
OTHER INFORMATION: (836)
OTHER INFORMATION: Human CD59 coding region.
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    Publication No. US20030086940A1
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US-10-225-19-25
; Sequence 25, Application US/1022519
; Publication No. US20030086940A1
; GENERAL INFORMATION:
; APPLICANT: Costa. Cristina
; APPLICANT: Costa. Cristina
; APPLICANT: Fodor, William L.
; TITLE OF INVENTION: AN ENGINEERED RECOMBINANT MOLECULE THAT REGULATES HUMORAL AND CEL
; TITLE OF INVENTION: AN ENGINEERED RECOMBINANT MOLECULE THAT REGULATES HUMORAL AND CEL
; TITLE OF INVENTION: AN ENGINEERED RECOMBINANT MOLECULE THAT REGULATES HUMORAL AND CEL
; TITLE OF INVENTION: AN ENGINEERE US 09/928,267
; FILE REFERENCE: 33-CIP 09-20
; FRIOR RAPLICATION NUMBER: US 09/928,267
; PRIOR FILING DATE: 2000-10-21
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SOFTWARE: PatentIn version 3.1
; SOFTWARE: PATENTIAL SEQUENCE
; TYPE: PRI
; VERNING ATLE: 200
; TYPE: PRI
; TYPE: PRI
; ORGANISM: Artificial Sequence
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NAME/KEY: misc_feature
LOCATION: (24)...(134)

OTHER INFORMATION: Porcine CTLA4 leader sequence.

NAME/KEY: misc_feature
LOCATION: (135)...(506)

OTHER INFORMATION: Porcine CTLA4 coding region.
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100.0%; Score 96; DB 14; Length 261;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels
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; OTHER INFORMATION: Human CD59 coding region.
US-10-225-519-25
LOCATION: (119)..(493)

TOTHER INFORMATION: CTLA4 coding region

NAME/KEY: misc_feature

LOCATION: (494)..(511)

THER INFORMATION: (G)6 linker region.

NAME/KEY: misc_feature

LOCATION: (512\)..(820)

COTHER INFORMATION: CD59 coding region

US-10-225-519-2
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LOCATION: (507)..(524)
OTHER INFORMATION: (AS)3 linker region.
NAME/KEY: misc_feature
LOCATION: (525)..(833)
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US-10-225-519-27
; Sequence 27, Application US/10225519
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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1 FEHCNFNDVTTRLRENE 17
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Maximum Match 100%
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	,	*			SUMMAKIES	
Result No.	Score	Query Match	Query Match Length DB	DB	П	Description
1	96	100.0	70	4.	US-09-612-314A-39	Sequence 39, Appl
7	96	100.0	71	4	US-09-612-314A-42	42,
m	96	100.0	77	4	US-09-612-314A-37	37,
4	96	100.0	82	4	US-09-612-314A-40	40,
Ŋ	96	100.0	83	4	US-09-612-314A-41	
9	96	100.0	103	Н	US-08-271-562-1	Ä
7	96	100.0	103	~	US-08-087-007-3	'n
80	96	100.0	103	~	US-08-696-777-1	۲,
6	96	100.0	103	٣	US-08-483-433-3	'n
10	96	100.0	103	ß	PCT-US92-05920-3	m
11	96	100.0	105	٣	US-09-591-435-12	12
12	96	100.0	115	4	US-09-513-999C-7845	78
13	96	100.0	115	4	US-09-513-999C-7846	7846,
14	96	100.0	115	4	US-09-513-999C-7847	7847,
15	96	100.0	128	9	5179198-1	. 51791
16	96	100.0	128	ø	5521296-1	Patent No. 5521296
17	96	100.0	128	9	5179198-1	Patent No. 5179198
18	96	100.0	128	9	5521296-1	Patent No. 5521296
19	96	100.0	135	4	US-09-949-016-9460	Seguence 9460, Ap
20	81	84.4	121	ო	US-09-591-435-13	13, A
21	46	47.9	294	4	US-09-252-991A-29464	
22	44	45.8	290	m	US-09-134-001C-4972	
23	43	44.8	15	4	US-09-835-752-1	
24	42.	43.8	203	4	US-09-270-767-58029	Sequence 58029, A
25	42	43.8	215	4	US-09-248-796A-21597	
26	42	43.8	404	4	-60-	14
27	42	43.8	415	4	US-09-248-796A-14912	Sequence 14912, A

Sequence 42, Application US/09612314A
Patent No. 6713606
GENERAL INFORMATION:
APPLICANT: SMITH, RICHARD ANTHONY GODWIN
APPLICANT: MOSSAKOWSKA, DANUTA EWA IRENA
TITLE OF INVENTION: CONJUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH
ITLE OF INVENTION: MEMBRANE-BINDING AGENTS
FILE REFERENCE: 37945-0004
CURRENT APPLICATION NUMBER: US/09/612,314A

US-09-612-314A-42

Sequence 42709, A Sequence 537, App Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 10, Appl Sequence 110, Appl Sequence 1134, A Sequence 1134, A Sequence 2, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 5, Appli Sequence 5, Appli Sequence 1, Appli	OMPOUNDS WITH	ence: Synthetic protein APT634 Length 70; Indels 0; Gaps 0;
3 4 US-09-270-767-42709 5 4 US-09-538-092-537 6 4 US-09-538-092-537 2 US-08-663-56A-15 2 US-08-023-610-15 2 US-08-023-610-15 2 US-08-023-610-15 2 US-08-028-065A-15 3 4 US-09-091-501B-10 3 4 US-09-091-501B-10 4 US-09-039-039A-11913 4 US-09-270-767-32551 4 US-09-270-767-32551 4 US-09-270-767-3757 1 US-08-277-231A-2 7 US-08-473-750-1	ALIGNMENTS -314A-39 W. 6713606 N. 6713606 I INFORMATION: CANT: SMITH, RICHARD ANTHONY GODMIN CANT: SMITH, RICHARD ANTHONY GODMIN CANT: BODD, IAN CANTION: MEMBRANE-BINDING AGENTS OF INVENTION: MEMBRANE-BINDING AGENTS OF INVENTION NUMBER: US 09/612,314A WIT FILING DATE: 1999-001-07 APPLICATION NUMBER: BCT/EP97/03715 FILING DATE: 1997-07-08 APPLICATION NUMBER: PCT/EP97/03715 FILING DATE: 1996-07-15 APPLICATION NUMBER: PCT/EP97/03715 FILING DATE: 1996-07-15 APPLICATION NUMBER: 1996-07-15	of Artificial Sequ Score 96, DB 4; Pred. No. 8.1e-09; ; Mismatches 0;
28 42 43.8 533 30 41 42.7 265 31 41 42.7 1162 32 41 42.7 1162 33 41 42.7 1162 34 41 42.7 1162 35 41 42.7 1162 36 41 42.7 1162 37 41 42.7 3433 39 40 41.7 3433 40 41.7 217 42 40 41.7 217 45 40 41.7 217	RESULT 1 US-09-612-314A-39 Sequence 39, Application US/09612314A Sequence 39, Application US/09612314A GENERAL INFORMATION: APPLICANT: SMITH, RICHARD ANTHONY GODWIN APPLICANT: DODD, IAN APPLICANT: MOSSAKOWSKA, DANUTA EWA IRENA ITILE OF INVENTION: WEMBRANE-BINDING AGEN CURRENT APPLICATION WHERE: US/09/612,314A CURRENT FILING DATE: 1999-03-16 PRIOR APPLICATION NUMBER: US/09/612,314A PRIOR PILING DATE: 1999-03-16 PRIOR FILING DATE: 1997-07-08 PRIOR FILING DATE: 1997-07-08 PRIOR FILING DATE: 1997-07-08 PRIOR FILING DATE: 1995-07-15 NUMBER OF SEQ ID NOS: 53 SEQ ID NO 39	LENGTH: 70 TYPE: PRT OCRGANISM: Artificial & FEATURE: OTHER INFORMATION: Det 09-612-314A-39 uery Match eet Local Similarity atches 17; Conservat atches 17; Conservat 1

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OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein APT2060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein APT635
US-09-612-314A-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: SMITH, RICHARD ANTHONY GODWIN
APPLICANT: DODD, IAN
APPLICANT: DODD, IAN
APPLICANT: DODD, IAN
TITLE OF INSOSAKOWSKA, DANUTA EWA IRENA
TITLE OF INVENTION: WEMBRANE-BINDING AGENTS
CURRENT APPLICATION NUMBER: US 09/214,913
PRIOR APPLICATION NUMBER: US 09/214,913
PRIOR PILING DATE: 1999-03-16
PRIOR PILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: GB 96 148 71.3
PRIOR APPLICATION NUMBER: GB 96 148 71.3
PRIOR APPLICANTION NUMBER: GB 96 148 71.3
SOFTWARE: PATENT NOS: 53
SOFTWARE: PATENT OF SEQ ID NOS: 53
IENGTH: 83
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100.0%; Score 96; DB 4; I
Best Local Similarity 100.0%; Pred. No. 9.7e-09;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 96, DB 4; I
Best Local Similarity 100.0%; Pred. No. 9.8e-09;
Matches 17; Conservative 0; Mismatches 0;
                           FILE REFERENCE: 37945-0004
CURRENT APPLICATION NUMBER: US/09/612,314A
CURRENT FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 09/214,913
PRIOR FILING DATE: 1999-03-16
PRIOR PILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: PCT/EP97/03715
PRIOR APPLICATION NUMBER: GB 6148 71.3
PRIOR FILING DATE: 1996-07-15
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 40
          TITLE OF INVENTION: MEMBRANE-BINDING AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 41, Application US/09612314A Patent No. 6713606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence 1, Application US/08271562; Sequence 1, 573940; Patent No. 5573940; GENERAL INFORMATION: APPLICANT: Sims, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 FEHCNFNDVTTRLRENE 59
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-612-314A-40
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US-09-612-314A-41
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                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein APT2061
US-09-612-314A-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic protein APT631
US-09-612-314A-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3. Application US/09612314A

Sequence 3. Application US/09612314A

Sequence 3. For 1366

GENERAL INFORMATION:

APPLICANT: SMITH, RICHARD ANTHONY GODWIN

APPLICANT: DODD, IAN

APPLICANT: DODD, IAN

APPLICANT: MOSSAKOWSKA, DANUTA EWA IRENA

TITLE OF INVENTION: WENERALE-BINDING AGENTS

FILE REFERENCE: 37945-0004

CURRENT APPLICATION NUMBER: US/09/612,314A

CURRENT PILING DATE: 1999-03-16

PRIOR FILING DATE: 1999-03-16

NUMBER OF SEQ ID NOS: 53

NUMBER OF SEQ ID NOS: 53

SOFTWARE: PARCET IN OF SEQ ID NOS: 53

SOFTWARE: PARCET IN OF SEQ ID NOS: 53

SOFTWARE: PARCET IN OF SEQ ID NOS: 53
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US-09-612-314A-40
; Sequence 40. Application US/09612314A
; Patent No. 6713606
; GENERAL INFORMATION:
; APPLICANT: SMITH, RICHARD ANTHONY GODWIN
; APPLICANT: DODD, IAM
; APPLICANT: MOSSAKOWAKA, DANUTA EWA IRENA
; TITLE OF INVENTION: CONJUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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100.0%; Score 96; DB 4; Length 77;
Best Local Similarity 100.0%; Pred. No. 9e-09;
Matches 17; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 17; Conservative 0; Mismatches 0; Indels
CURRENT FILING DATE: 2000-07-07
PRIOR APPLICATION WUNBER: US 09/214,913
PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1997-07-08
PRIOR FILING DATE: 1997-07-08
PRIOR FILING DATE: 1997-07-08
PRIOR FILING DATE: 1996-07-15
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.1
LENGTH: 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 FEHCNFNDVTTRLRENE 58
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-612-314A-37
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LENGTH: 77
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GENERAL INVORMATION:

APPLICANT: Sims, Peter, J.

APPLICANT: Sims, Peter, J.

TITLE OF INVENTION: Genetic Inhibition of Complement Mediated

TITLE OF INVENTION: Inflammatory Response

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Patrea L. Pabst

STREET: 2800 One Atlantic Center, 1201 West Peachtree Street

CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                           COMPUTER READABLE FORM:

STATE: Georgia

COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPY disk

COMPUTER: IBM PC COMPATIOLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/087,007

FILING DATE: 19930701

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Pabst, Patrea L.

REFERENCE/DOCKET NUMBER: 31,284

REPRENCE/DOCKET NUMBER: 31,284

REFERENCE/DOCKET NUMBER: 31,284

REPRENCE/DOCKET NUMBER: 31,284
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FILLOALICATION NUMBER: US/08/696,777
FILING DATE: 13-AUG-1996
                               E: Kilpatrick & Cody
1100 Peachtree Street, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 1, Application US/08696777; Patent No. 5955441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 103 amino acide
TYPE: amino acid
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETIZAL: NO
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ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-terminal
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IMMEDIATE SOURCE:
CLONE: CD59
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     CORRESPONDENCE ADDRESS:
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Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                  ADDRESSEE:
STREET: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-087-007-3
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APPLICANT: Bothwell, Alfred L.M.
ITILE OF INVENTION: Genetic Inhibition of Complement
ITILE OF INVENTION: Mediated Inflammatory Response
                                                                                                                                                                                                                 STATE: Georgia
CONNTRY: U.S.
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/271,562
FILING DATE:
                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Madri, Joseph
APPLICANT: Rollins, Scott
APPLICANT: Bell, Leonard
APPLICANT: Squinto, Stephen
TITLE OF INVENTION: Universal Donor Cells
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Paber, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF 112CIP
TELECOMMUNICATION INFORMATION:
TELEPAN: (404) 815-6508
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/729926
FILING DATE: 15-JUL-1991
APPLICATION NUMBER: US 07/365199
FILING DATE: 04-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sims, Peter J.
Bothwell, Alfred L.M.
Elliott, Eileen A.
Flavell, Richard A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08087007; Patent No. 5705732; Patent No. 5705732 5684223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEHCHFNDVTTRLRENE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 103 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE TYPE: Blood
CELL TYPE: Erythrocyte
US-08-271-562-1
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Best Local Similarity 100.
Matches 17, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Sims, Pe
APPLICANT: Bothwell
APPLICANT: Eliott,
APPLICANT: Flavell,
                                                                                                                                                                                               CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
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US-08-087-007-3
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                                                                                                                                                                                                 Length 103;
                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05920
FILING DATE: 19920714
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: PabSt, PROFE 31, 284
REGISTRATION NUMBER: 31, 284
REFERENCE/DOCKET NUMBER: 0MRF135
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: 404-815-6555
                                                                                                                                                                                               Query Match
100.0%; Score 96; DB 3; I
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sims, Peter J.
APPLICANT: State, Alfred L.M.
APPLICANT: Bliott, Elleen A.
APPLICANT: Flavell, Richard A.
APPLICANT: Madri, Joseph
APPLICANT: Madri, Joseph
APPLICANT: Madri, Leonard
APPLICANT: Squinto, Stephen
ITLE OF INVENTION: Universal Donor Cells
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: Kilpatrick & Cody
1100 Peachtree Street, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONTRY: U.S.
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application PC/TUS9205920 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                    42 FEHCNFNDVTTRLRENE 58
                                                                                                                                                                                                                                                                                          1 FEHCNFNDVTTRLRENE 17
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
       AVI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CTONE: CD59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 103 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-terminal
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IMMEDIATE SOURCE:
CLONE: CD59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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STATE: Georgia
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ORIGINAL SOURCE:
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HYPOTHETICAL:
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                                                                                                                                                     US-08-483-433-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.

COUNTRY: U.S.

ZIP: 30309-3450

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,433
              ATTORNEY AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 0MF 112cipdiv
TELECOMMUNICATION INFORMATION:
TELEPAX: (404)-873-8794
TELEPAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OMRF135cip2 div
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TITLE OF INVENTION: Universal Donor Cells
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSES: Patrea L. Pabst
STREET: 2800 One ALlantic Center
STREET: 1201 West Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/087,007
FILING DATE: July 1, 1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/906,394
FILING DATE: June 29, 1992
CLASSIFICATION NUMBER: 91, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 0MRF1356
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
US-08-483-433-3
US-08-483-433-3
Sequence 3, Application US/08483433
Patent No. 6100443
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FEHCNFNDVTTRLRENE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 FEHCNFNDVTTRLRENE 58
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: peptide US-08-696-777-1
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Atlanta
STATE: Georgia
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FACELIA NO. 903501.

APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.

APPLICANT: Duclert, A.

APPLICANT: Duclert, A.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

PALENT: PLINE DATE: 2000-02-24

CURRENT PILING DATE: 2000-02-24

FRIOR PLING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: PATENTE PATE
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APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT PILING DATE: 2000-02-24
PRIOR PILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 7847
LENGTH: 115
TYPE: PRT
ORGANISM: Homo sapiens
                                                                      Gaps
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   Length 115;
                                                                   Indels
   Score 96; DB 4; I
Pred. No. 1.4e-08;
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100.0%; Score 96; DB 4; I
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 17; Conservative 0; Mismatches 0;
Query Match 100.0%; Score 96; DB Best Local Similarity 100.0%; Pred. No. 1.4 Matches 17; Conservative 0; Mismatches
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; OTHER INFORMATION: score 10.4
; OTHER INFORMATION: seq VLFGLLLVLAVFC/HS
US-09-513-999C-7847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: -20..-1
; OTHER INFORMATION: score 10.4
; OTHER INFORMATION: seq VLFGLLLVLAVFC/HS
US-09-513-999C-7846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7847, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                           Sequence 7846, Application US/09513999C Patent No. 6783961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FEHCNFNDVTTRLRENE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 FEHCNFNDVTTRLRENE 83
                                                                                                                                         1 FEHCNFNDVTTRLRENE 17
                                                                                                                                                                                                     67 FEHCNFNDVTTRLRENE 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SIGNAL
                                                                                                                                                                                                                                                                                                        RESULT 13
US-09-513-999C-7846
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TITLE OF INVENTION: METHODS TO IDENTIFY POLYNUCLECTIDE AND POLYPEPTIDE

TITLE OF INVENTION: BEQUENCES WHICH MAY BE ASSOCIATED WITH PHYSIOLOGICAL

TITLE OF INVENTION: AND MEDICAL CONDITIONS

TITLE OF INVENTION: AND MEDICAL CONDITIONS

FILE REFERENCE: GENO. 200. 2

CURRENT APPLICATION NUMBER: US/09/591,435

CURRENT APPLICATION NUMBER: 09/591,435

PRIOR FILING DATE: 2000-06-09

PRIOR FILING DATE: 1999-01-29

PRIOR FILING DATE: 1999-01-29

PRIOR FILING DATE: 1998-01-30

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PATENTIN VET. 2.0
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; Sequence 7845, Application US/09513999C
; Patent No. 678364
; Patent No. 678364
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; PATEL OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; PILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT APPLICATION NUMBER: US 60/122,487
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SEQ ID NO 7845
; LENGTH: 115
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       Indels
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   Mismatches
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; THEN INFORMATION: SCORE 10.4
; OTHER INFORMATION: SEG VLFGLLLVLAVFC/HS
US-09-513-9990C-7845
                                                                                                                                                                                                                                                                                                        ; Sequence 12, Application US/09591435; Patent No. 6280953; GENERAL INFORMATION: ; APPLICANT: MESSIER,
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEHCNFNDVTTRLRENE 59
                                                                      1 FEHCNFNDVITTRERE 17
                                                                                                                    FEHCNFNDVTTRLRENE
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   17; Conservative
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Best Local Similarity
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LOCATION: -20..-1
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US-09-591-435-12
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       Matches
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  Length 115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 96; DB 6; Length 128; 100.0%; Pred. No. 1.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: OKADA, HIDECHIKA,OKADA, NORIKO,NACAMI, YOICHI,
TTILE OF INVENTION: GLYCOPROTEIN AND GENE CODING THEREFOR
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/739,211
FILING DATE: 01-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION DATE:
APPLICATION NUMBER: 376,828
FILING DATE: 07-JUL-1989
                                                                                                                                                                                                                                               APPLICANT: OKADA, HIDECHIKA; OKADA, NORIKO; NAGAMI, YOICHI; TAKASHI, KAZUHIRO; TAKIZAWA, HISAO; KONDO, JUN
TITLE OF INVENTION: GLYCOPROTEIN AND GENE CODING THEREFOR NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/376,828
FILING DATE: 07-JUL-1989
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'TAKASHI, KAZUHIRO,TAKIZAWA, HISAO,KONDO, JUN
TITLE OF INVENTION: GIVCOPROTEIN AND GENE CODING THEREFOR
NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
APPLICATION UNDRER: US/O7/376,828
FILING DATE: 07-JUL-1989
                                           0; Indels
Score 96; DB 4; I
Pred. No. 1.4e-08;
); Mismatches 0;
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                                                                               1 FEHCNFNDVTTRLRENE 17
                                                                                                            67 FEHCNFNDVTTRLRENE 83
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 17; Conservative 0
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Matches 17; Conservative
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;Patent No. 5179198
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                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 128
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co-vy-vy-ub-yapulcation US/09949016

patent No. 681239

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APLICATION NUMBER: (0/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 128;
                                                                                                                                                                                                                              PARENT NO. 5521296

PAPLICANT: OKADA, HIDECHIKA,OKADA, NORIKO,NAGAMI, YOICHI,
TAKAHASHI, KAZUHIRO,TAKIZAWA, HISAO,KONDO, JUN
TITLE OF INVENTION: GLYCOPROTEIN AND GENE CODING THEREFOR
WUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
PILING DATE: 01-AUG-1991
PRICA PAPLICATION NUMBER: 376,828
FILING DATE: 07-JUL-1989
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Query Match 100.0%; Score 96; DB 6; I
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 17; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pr
Matches 17; Conservative 0;
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Job time: 42 secs
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US-09-949-016-9460
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June 8, 2005, 10:57:53; Search time 38 Seconds (without alignments) 43.044 Million cell updates/sec
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                       OM protein - protein search, using sw model
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US-09-020-393B-3_COPY_42_58 96

1 FEHCNFNDVTTRLRENE 17 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 17

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	latostatin - t	fibrinogenolytic p	urinary tract ston	transaldolase (EC	hypothetical prote	somatostatin precu	alpha-conotoxin Ep		hypothetical prote	botulinum neurotox	aldehyde dehydroge	alcohol dehydrogen	transaldolase (EC	proteochondoitin c	. GTP-binding protei		seed storage prote	bombolitin IV - Am	Ig heavy chain CRD	peptidylglycine mo	T-cell receptor be	aminotransferase c	Ig H chain V-D-J r	H+-transporting tw	ribosomal protein	photosystem II chl	cal p		hypothetical prote
SUMMARIES	a	161	PC2215	H56046	A11497	PS0371	A61117	A59042	G49039	T46794	S08575	152226	871919	A12872	PT0077	S29486	832677	PA0009	D22595	PT0272	A42266	PH0895	PC2124	PH1627	PT0095	836889	S20490	208606	PT0284	S27873
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	Query Match Length	1	15	13	თ	14	17	16	16	12	13	16	œ	6	14	14	15	15	17	σ	6	10	. 11	14	15	15	17	7	10	10
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	Score	7	25	24	23	23	23	22	22	21	21	21	20	20	20	20	20	20	20	19	19	19	19	19	19	19	19	18	18	18
	Result No.	-	7	e	4	Ŋ	9	7	89	60	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

seed protein ws-17 urinary tract ston carbonic anhydrase Ig heavy chain DJ Ig H chain V-D-J r 25K elastin-bindin lectin Bl - psopho placental calcium- Ig heavy chain CDR Ig heavy chain DJ lectin A3 - Psopho lectin A3 - Psopho lectin A3 - Psopho	alpha-conocoxin Mi T cell receptor al vespulakinin 1 - e
B61497 G56046 PH1347 PH1625 PH1625 A41589 A41589 PA0007 PT0222 PH1310 PA0006 PA0006	A59046 PH1778 A61339
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0 H 2 E E E E E E E E E E E E E E E E E E	4 4 4 ህ 4 7

ALIGNMENTS

A61612

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C;Accession: A61612
R;Kramer, S.J.; Toschi, A.; Miller, C.A.; Kataoka, H.; Quistad, G.B.; Li, J.P.; Carney, Proc. Natl. Acad. Sci. US.A. 88, 9458-9462, 1991
A;Title: Identification of an allatostatin from the tobacco hornworm Manduca sexta.
A;Reference number: A61612; MUID:92052112; PMID:1946159
allatostatin - tobacco hornworm
C;Species: Manduca sexta (tobacco hornworm)
C;Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                 A,Accession: A61612
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <KRA>
A;Cross-references: UNIPROT:P42559
C;Keywords: neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
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Gaps .. 29.2%; Score 28; DB 2; Length 15; 40.0%; Pred. No. 2.8e+02; tive 2; Mismatches 4; Indels 4; Conservative Best Local Similarity Matches 4; Conserv Query Match

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4 FRQCYFNPIS 13 1 FEHCNFNDVT 10 셤 Š

fibrinogenolytic proteinase A2 (EC 3.4.21.-) - western diamondback rattlesnake (fragment NALlerante names: alpha-fibrinogenase A2 C;Species: Crotalus atrox (western diamondback rattlesnake)
C;Species: Crotalus atrox (western diamondback rattlesnake)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C,Accession: PC2215 R,Hung, C.C.; Chiou, S.H. Biochem. Biophys. Res. Commun. 201, 1414-1423, 1994 A,Tltle: Isolation of multiple isoforms of alpha-fibrinogenase from the western diamondb

A; Reference number: PC2214; MUID: 94296418; PMID: 8024586 A; Accession: PC2215

A; Molecule type: protein A; Residues: 1-15 < HUN>

A, Cross-references: UNIPROT: 09PRW3 C, Superfamily: trypsin; trypsin homology C, Keywords: hydrolase; serine proteinase

Gaps ö Query Match 26.0%; Score 25; DB 2; Length 15; Best Local Similarity 42.9%; Pred. No. 8.5e+02; Matches 3; Conservative 2; Mismatches 2; Indels

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EHCNFND 8 : || |: N

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R. Loughman, M.; Bond, T.; Atkins, A.; Cuevas, J.; Adams, D.J.; Broxton, N.M.; Livett, B.C. Biol. Chem. 273, 15667-15674, 1998
A. Title: Alpha-conotoxin EpI, a novel sulfated peptide from Conus episcopatus that selection A, Reference number: A59042; MUID:98288307; PMID:9624161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Superfamily: alpha-conotoxin
C; Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neurotor
F;1-16/Product: alpha-conotoxin Epi #status experimental <MAT>
F;2-8,3-16/Disulfide bonds: #status experimental
F;15/Binding site: sulfate (Tyr) (covalent) #status experimental
F;15/Modified site: amidated carboxyl end (Cys) #status experimental
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R;Rosenberg, W.W.; Moss, P.A.; Bell, J.I.

Bur. J. Immunol. 22, 541-549, 1992
A;Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using A;Reference number: A49039; MUID:92164737; PMID:1311263
                                                                                                                                                                                                                                   C,Accession: A61117
R;Mackin, R.B.; Noe, B.D.; Spiess, J.
Rimackin, R.B.; Noe, B.D.; Spiess, J.
Rimackin, R.B.; Noe, B.D.; Spiess, J.
Ridoctinology 129, 2263-2265, J.
A;Tit.le: Identification of a somatostatin-14-generating propeptide converting enzyme as A;Reference number: A61117; MUID:92007528; PMID:1680673
A;Accession: A61117
A;Molecule type: protein
A;Residues: 1-17 <MAC>
                                                                                                                                                           somatostatin precursor processing enzyme (EC 3.4.21.-) - American goosefish (fragment)
C,Species: Lophius americanus (American goosefish)
C,Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 13-Sep-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor beta chain V-D-J-C region (V beta 4, J beta 2.2) - human (fragment)
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C;Species: Conus episcopatus (bishop's cone)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
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C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
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Pred. No. 2.8e+03;
1; Mismatches 1; Indels
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Pred. No. 2.1e+03;
3; Mismatches 5;
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C, Superfamily: kexin; subtilisin homology
C, Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 cLOU>
A;Cross-references: UNIPROT: P56638
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Best Local Similarity 27.3%;
Matches 3; Conservative
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                         7 DVTGRLQ 13
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hypothetical protein (psaC region) - Synechococcus sp. (fragment)
c;Species: Synechococcus sp.
c;Accession: PS0371
R;Rhiel, E.; Stirewalt, V.L.; Gasparich, G.E.; Bryant, D.A.
dene 112, 123-128, 1992
A;Title: The psaC genes of Synechococcus sp. PCC7002 and Cyanophora paradoxa: cloning an A;Reference number: JS0694; MUID:92201692; PMID:1551590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arch. Biochem. Biophys. 167, 525-533, 1975
A;Title: Isolation of a peptide containing a histidinyl-cysteinyl sequence from the acti
A;Reference number: A11497; MUID:75145197; PMID:1092268
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                                                                                                                              Usinary tract stone matrix protein 10, 42K - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: H56046
R;Binette, J.P.; Binette, M.B.; Gawinowicz, M.A.; Kendrick, N.
submitted to the Protein Sequence Database, February 1995
A;Description: Isolation, characterization and sequence of stone proteins.
A;Reference number: A56046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transaldolase (BC 2.2.1.2) III - yeast (Pichia jadinii) (fragment)
C;Species: Pichia jadinii, Candida utilis
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C;Accession: Al1497
R;Tsolas, O.; Sun, S.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 1.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 24; DB 2; Length 13;
Pred. No. 1.1e+03;
1; Mismatches 2; Indels
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A,Molecule type: protein
A,Rossidues: 1-9 < 750>
A,Cross-references: UNIPROT:P17441
C,Keywords: transferase
                                                                                                                                                                                                                                                                                                                                                                                      A Status: preliminary
A,Molecule type: protein
A,Residues: 1-13 <BIN>
A;Cross-references: UNIPROT:Q7M4P7
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57.1%;
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Best Local Similarity 71.44
Thes 5; Conservative
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Matches 4; Conservative
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DECNINE 11
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A; Residues: 1-14 <RHI>
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Biochem. Biophys. Res. Commun. 152, 940-947, 1988

A;Title: Characterization of a functional recombinant rat liver aldehyde dehydrogenase: F
A;Reference number: 152226; MUID:88209084; PMID:3284529
A;Accession: 152226
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-16 <RES>
A;Cross-references: UNIPROT:Q63039; GB:M29320; NID:g202853; PIDN:AAA40722.1; PID:g202854
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alcohol dehydrogenase (EC 1.1.1.1) - grass carp (fragment)
Cispecies: Ctenopharyngodon idella (grass carp)
Cipate: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 09-Jul-2004
CjAccession: 871919
R;Tsui, H.T.; Mock, W.Y.; Lau, K.K.; Fong, W.P.
Biochim. Blophya. Acta 1996, 4-146, 1996
A;Title: Proteolytic activation of grass carp (Ctenopharygodon idellus) liver alcohol dei A;Reference number: 871919; MUID:96350418; PMID:8765227
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R;Sun, S.C.; Joris, L.; Tsolas, O.
Arch. Biochem. Biophys. 178, 69-78, 1977
A;Title: Purification and crystallization of transaldolase isozyme I and evidence for di A;Reference number: A12872; MUID:77110646; PMID:556924
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C,Species: Pichia jadinii, Candida utilis
C,Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
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A;Note: the source is designated Ctenopharyngodon idellus
C;Keywords: NAD; oxidoreductase
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66.7%; Pred. No. 2.8e+05;
cive 1; Mismatches 0;
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A;Residues: 1-9 <SUN>
A;Cross-references: UNIPROT:P17440
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Best Local Similarity 66.7
Matches 4; Conservative
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Matches 4; Conservative
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A;Molecule type: protein
A;Residues: 1-8 <TSU>
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Matches 2; Conserv
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PT0077
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A;Title: Nucleotide sequence of four genes encoding ribosomal proteins from the 'S10 and A;Reference number: S10731; MUID:90336772; PMID:2143141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: UNIPROT: P10971; EMBL: X55311; NID: 943610; PIDN: CAA39015.1; PID: 943614
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A;Residues: 1-13 <SCH>
A;Cross-references: UNIPROT;Q00496
Experimental source: strain Alaska E-43
F;1-13/Product: botulinum neurotoxin E light chain (fragment) #status predicted <LIG>
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Dotulinum neurotoxin type E - Clostridium botulinum (strain Alaska E-43) (fragment)

Dotulinum neurotoxin type E - Clostridium botulinum

A, Variety: strain Alaska E-43

C, Spacie: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004

C, Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004

C, Accession: S08575

A, Sathyamoorthy, V.; DasGupta, B.R.

A, Schmidt, J.J.; Sathyamoorthy, V.; DasGupta, B.R.

A, Schmidt, J.J.; Sathyamoorthy, V.; DasGupta, B.R.

A, Strine: Partial amino acid sequences of botulinum neurotoxins types B and E.

A, Reference number: S01128, MUID:85197963; PMID:3888113
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Pattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: 152226
R;Harper, K.; Jones, D.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein [imported] - Haloarcula marismortui (fragment)
C;Species: Haloarcula marismortui
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004
C;Accession: T46794
R;Arndt, E.
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                                                                                                                                         Length 16;
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80.0%; Pred. No. 3e+03;
tive 1; Mismatches 0; Indels
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                                                                                                                                                                                              Indels
     A;Molecule type: nucleic acid
A;Residues: 1-16 <ROS>
A;Note: sequence extracted from NCBI backbone (NCBIP:90719)
C;Keywords: T-cell receptor
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                                                                                                                                      / Match 22.9%; Score 22; DB 2; I Local Similarity 41.7%; Pred. No. 2.8e+03; les 5; Conservative 1; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-12 <ARN>
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LQENE 12
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7 NYND 10
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Matches
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proteochondoitin core protein - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Species: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 04-Sep-1998
C;Accession: PT0077
R;Accession: PT0077
R;Accession: PT0077
R;Marcum, J.A.; Thompson, M.A.
Biochem. Biophys. Res. Commun. 175, 706-712, 1991
A;Title: The amino-terminal region of a proteochondroitin core protein, secreted by aort on human bone.
A;Reference number: PT0077; MUID:91207372; PMID:2018513
A;Accession: PT0077
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Holecule type: protein
A;Residues: 1-14 *MAR>
C;Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan
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329486
GTP-binding protein o-rab3 - electric ray (Discopyge ommata) (fragment)
C;Species: Discopyge ommata
C;Species: Discopyge ommata
C;Date: 22-Nov-1993 #sequence_revision 27-Feb-1997 #text_change 13-Mar-1997
C;Accession: S29486
R;Volknandt, W.; Pevener, J.; Elferink, L.A.; Scheller, R.H.
R;Volknandt, W.; Dasser, J.; Elferink, L.A.; Scheller, R.H.
R;EBS Lett. 317, 53-56, 1993
A;Title: Association of three small GTP-binding proteins with cholinergic synaptic vesic A;Reference number: S29486
A;Reference number: S29486
A;Recession: S29486
A;Recession: S29486
A;Recession: Preliminary
A;Residues: 1-14 <VOL>
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(c) 1993 - 2005 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 44, Last annotation update)
Allatostatin (Mas-AS).
Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Sphingidae; Sphinginae; Manduca.
MCBI_TaxID=7130;
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MEDLINE=92052112; PubMed=1946159;
Kramar S.J., Toschi A., Miller C.A., Kataoka H., Quistad G.B.,
Li J.P., Carney R.L., Schooley D.A.;
"Identification of an allatostatin from the tobacco hornworm Manduca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Proc. Natl. Acad. Sci. U.S.A. 88:9458-9462(1991).
-!- FUNCTION: Strongly inhibits juvenile hormone biosynthesis
by the corpora allata from fifth-stadium larvae and adult
-!- SIMILARITY: Belongs to the allatostatin family.
0719k4
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IncN plasmid pKM101.
other sequences; broad host range plasmids.
NCBI_TaxID=192122;
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Best Local Similarity
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Gaps

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Q8WMM1;

Q8WM1

Matches

RL PR SO FT

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Hung C.C., Chiou S.H.;
"Isolation of multiple isoforms of alpha-fibrinogenase from the
Western diamondback rattlesnake, Crotalus atrox: N-terminal sequence
homology with ancrod, an antithrombotic agent from Malayan viper.";
Blochem. Blochew. Bophys. Res. Commun. 201:1414-1423(1994).
SEQUENCE 15 AA; 1656 MW; 03EFE10227D52FDA CRC64;
                                                                                  InterPro; IPR001254; Peptidase_S1.
PROSITE; PS0240; TRYPSIN DOM; PARTIAL.
PROSITE; PS00134; TRYPSIN HIS; PARTIAL.
PROSITE; PS00135; TRYPSIN HIS; PARTIAL.
Direct protein sequencing; Glycoprotein; Hydrolase; Serine protease.
15 As; 1642 MW; 03EFE10227CD8CDA CRC64;
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"Isolation of multiple isoforms of alpha-fibrinogenase from the
"Nestern diamondback rattlesnake, Crotalus atrox: N-terminal sequence
homology with ancrod, an antithrombotic agent from Malayan viper.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Epidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Crotalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Crotalus atrox (Western diamondback rattlesnake).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eupidosauvia, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Crotalus.
  -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- SIMILARITY: Belongs to the peptidase S1 family. Snake venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 25; DB 2; Length 15; Pred. No. 3.4e+03; 2; Mismatches 2; Indels
                                                                                                                                                                                                                                             Score 25; DB 1; Length 15; Pred. No. 3.4e+03; 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2000 (TrEMBLrel. 13, Last annotation update)
Alpha-FIBRINOGENASE isoform A3 (Fragment).
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
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Alpha-FIBRINOGENASE isoform A2 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94296418; PubMed=8024586;
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42.9%;
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42.9%;
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5 DECNINE 11
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5 DECNINE 11
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Matches 3; Conserv
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Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                 2 EHCNFND 8
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                                                                   subfamily
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-!- CATALYTIC ACTIVITY: Selective cleavage of Arg-|-Xaa bond in fibrinogen, to form fibrin, and release fibrinopeptide A. The specificity of further degradation of fibrinogen varies with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pāllas).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Gloydius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (Rel. 44, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Ancrod (EC 3.4.21.74) (Venombin A) (Protein C activator) (ACC-C)
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Pred. No. 1.4e+03;
3; Mismatches 2; Indels
                                                                                                    Score 28; DB 2; Length 16;
Pred. No. 1.2e+03;
2; Mismatches 2; Indels
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF000361; AABS8710.1; -.
NON_TER 16 16
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ492142; CAD21106.1; -..
GO; GO:0008233; F:peptidase activity; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 AA; 1586 MW; 6C8D835C06AB72CB CRC64;
                                                                 49BCB8ESECBD5CE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
03-dipain-like protease (Fragment).
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Submitted (FEB-1997) to Swiss-Prot.
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(Rel. 44, Last seq
                                                                                                       29.2%;
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                                                               16 AA; 1791 MW;
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Les 5; Conservative
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| SEVPVQLRE 13
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                                                                                                                              Best Local Similarity
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P80899;
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RESULT 4 VSP3_AGKHP

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2; Indels

Score 24; DB 2; I Pred. No. 4.3e+03; 1; Mismatches 2;

Length 13;

0A219099F5D32AA4 CRC64;

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25.0%;
57.1%;
                                                        1483 MW;
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NFNEKLSQLQ 11
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  PIR; H56046; H56046.
NON_TER 1 1 13
NON_TER 13 13
SEQUENCE 13 AA; 148
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PubMed=12582899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=APOB;
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Q9AXV9;
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                                                                                                                       Gaps
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MEDLINE=92005680; PubMed=1717157; DOI=10.1016/0092-8674(91)90051-Y;
Coulombe P., Hutton M., Letai A., Hebert A., Paller A., Fuchs E.;
"Point mutations in human keratin 14 genes of epidermolysis bullosa simplex patients: genetic and functional analyses.";
Cell 66:1301-1311(1991).
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Q7M4P7;

Q1-MAR-2004 (TrEMBLrel. 26, Last sequence update)

01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

Urinary tract stone matrix protein 10, 42K (Fragment).

Uninary tract stone matrix protein 10, 42K (Fragment).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Binette J.P., Binette M.B., Gawinowicz M.A., Kendrick N.;
Submitted (FEB-1995) to the PIR data bank.
                                                                             26.0%; Score 25; DB 2; Length 15; 42.9%; Pred. No. 3.46+03; Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.0%; Score 24; DB 2; Length 9; 100.0%; Pred. No. 1.6e+06; tive 0; Mismatches 0; Indels
                                          03EFE10227CA12DA CRC64;
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9 AA; 1138 MW; BE300AA449C456D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
Biochem. Biophys. Res. Commun. 201:1414-1423(1994)
PIR; PC2215; PC2215.
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EMBL; D28807; BAA05967.1; -.
GO; GO:0005882; C:intermediate filament; NAS.
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                                                                                                                                                                                                                                                                                                                                                  Created)
          PIR; PC2215; PCZZIS.
                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 01,
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                                                                                                Local Similarity 42.9
nes 3; Conservative
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01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                         Keratin 14 (Fragment).
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DECNINE 11
                                                                                                                                                             2 EHCNFND 8
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Q7M4P7
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"From Arabidopsis thaliana to Brassica napus: development of amplified consensus genetic markers (ACGM) for construction of a gene map."; Theor. Appl. Genet. 105:1196-1206 (2002).
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=88018019; PubMed=3659919;
Chen S.-H., Habib G., Yang C.-Y., Gu Z.-W., Lee B.R., Weng S.-A.,
Silberman S.R., Cai S.-J., Deslypere J.P., Rosseneu M.,
Gotto A.M.Jr. ., Li W.-H., Chan L.;
"Apolipoprotein B-48 is the product of a messenger RNA with an organ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Surosids II; Brassicales; Brassicaceae; Brassica.
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                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                         01-MAY-1997 (TrEMBLrel. 03, Created)
1-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
APOB protein (Fragment).
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
Phytochrome A (Fragment).
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Science 238:363-366(1987).
EMBL; M18036; AAA51754.1;
PIR; A27850; LPHUB.
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Gaps

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Score 24; DB 2; Length 16;
Pred. No. 5.4e+03;
1; Mismatches 3; Indels
                                                                                                     6C1E698806AEE77B CRC64;
    J. Clin. Microbiol. 42:2455-2460(2004).
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                    EMBL; AY329569; AAQ95940.1; -. InterPro; IPR000236; TransactX.
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SEQUENCE 16 AA; 1896 MW;
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Sitnik R., Rebello Pinho J.R., Bertolini D.A., Bernardini A.P.,
Da Silva L.C., Carrilho F.J.;
"Hepatitis B virus genotypes and precore and core mutants in brazilian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "From Arabidopsis thaliana to Brassica napus: development of amplified consensus genetic markers (ACGM) for construction of a gene map."; Theor. Appl. Genet. 105:1196-1206 (2002).
EMBL; AF229413; AAK00685.11; GO; GO:0008020; F:G-protein coupled photoreceptor activity; IEA. GO; GO:0008855; P:red, far-red light phototransduction; IEA. Phytochrome.
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Fourmann M., Barret P., Froger N., Baron C., Charlot F., Delourme R.,
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GO; GO:0008020; F:G-protein coupled photoreceptor activity; IEA.
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05-JUL-2004 (TrEMBLrel. 27, C;
05-JUL-2004 (TrEMBLrel. 27, Ls
X protein (Fragment).
Hepatitis B virus.
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16 AA; 1819 MW;
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Brassica napus (Rape).
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MEDLINE=9547658; PubMed=7730255;
Dervyn E., Poncet S., Klier A., Rapoport G.;
Dervyn E., Poncet S., Klier A., Rapoport G.;
Transcriptional regulation of the cryIVD gene operon from Bacillus thuringiensis subsp. israelensis.";
J. Bacteriol. 177:2283-2291(1995).
EMBL; S78174; AAB34195.1; -.
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SEQÜENCE 17 AA, 2052 MW; 085F1686F7987A08 CRC64;
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Neopiera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
Andrenidae; Andreninae; Andrena.
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                                                                                                                                                                                                                                     Bacillús thuringiensis.
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1428;
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                                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Cytochrome oxidase subunit I (Fragment).
17 AA.
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MEDLINE=75145197; PubMed=1092268;

Taolas O., Sun S.C.; representation of a peptide containing a histidinyl-cysteinyl sequence of translation of a peptide containing a histidinyl-cysteinyl sequence of from the active center of transladolase.";

Arch. Biochem. Biophys. 167:525-531(1975).

-!- FUNCTION: Transladolase is important for the balance of metabolites in the pentose-phosphate pathway.

-!- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde 3-phosphate = D-erythrose 4-phosphate + D-fructose 6-phosphate.

-!- PATHWAY: Pentose phosphate pathway; nonoxidative part.

-!- SIMILARITY: Belongs to the transaldolase family. Subfamily 1.

PIR; Al1497; Al1497; Arnsaldolase.

R InterPro: IPRO01585; Transaldolase.

R PROSITE; PS001054; TRANSALDOLASE 1; PARTIAL.

R PROSITE; PS00958; TRANSALDOLASE 2; PARTIAL.

R PROSITE; PS00958; TRANSALDOLASE 2; PARTIAL.

M Direct protein sequencing; Pentose shunt; Transferase.
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TAL3 PICJA

ID TAL3 PICJA

AC P1741;

DT 101-AUG-1990 (Rel. 15, Last sequence update)

DE Transladolase III (EC 2.2.1.2) (Fragment)

OS Saccharomycetales; Saccharomycotina; Saccharomycotina; Saccharomycetales; Saccharomycotina; Saccharomycetales; Saccharomycotina; Saccharomycotina; Saccharomycetales; Saccharomycotina; Saccharomycetales; Saccharomycotina; Saccharomycotina; Rx MEDLINE=75145197; PubMed=1092268;

RX MEDLINE=75145197; PubMed=1092268;

RX Tisolation of a peptide containing a histidinyl-cysteinyl sequence
RT from the active center of transaldolase.";

Arch. Biochem. Biophys. 167:525-533(1975).

CC --- FUNCTION: Transaldolase is important for the balance of metabolites in the pentose-phosphate pathway, nonoxidative part.

CC --- STMILANTY: Belongs to the transaldolase family. Subfamily 1.

DR RNOSITE; PSO1056; TRANSALDOLASE 1; PARTIAL.

EN PROSITE; PSO1056; TRANSALDOLASE 2; PARTIAL.

EN PROSITE; PSO0956; TRANSALDOLASE 2; PARTIAL.

EN PROSITE; PSO0956; TRANSALDOLASE 2; PARTIAL.

EN PROSITE; PSO0956; TRANSALDOLASE 2; PARTIAL.

EN PROSITE: PSO0956; TRANSALDOLASE 2; PARTIAL.

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Best Local Similarity 26.7%; Pred. No. 5.7e+03; Matches 4; Conservative 6; Mismatches 4
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SUMMARIES

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Description	Adr38586 Human CD5	Aab67300 Cytokine	Abb56683 Human SNP	Adm33098 Human imm	Abp82501 G protein					٠.	1 Virus	Adk70613 Human ery	Adk70612 Human ery	Adk70576 Human ery	Adk70658 Human ery	Adn65159 HLA bindi	Aar70779 EPO neuro	Adi38855 Human ery	Aaw30024 Cytokine	_	Adq94321 Human pre	Ade28574 Human CD1	Human	Abb83992 Human pho	Abj04349 Human col
ID	ADR38586	AAB67300	ABB56683	ADM33098	ABP82501	AAY58596	ADC17406	ADC17402	ADR18924	ADR18928	AAR83971	ADK70613	ADK70612	ADK70576	ADK70658	ADN65159	AAR70779	ADI38855 ,	AAW30024	AAW66142	ADQ94321	ADE28574	AAM97385	ABB83992	ABJ04349
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2 1 1 1 1 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1	12
	30.2
7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	29
0 C C C C C C C C C C C C C C C C C C C	45

ALIGNMENTS

Human, CD59; protein glycation; diabetes mellitus; urine; immunogen; blood sugar; glycaemic control. /note= "Optionally Glycated" Location/Qualifiers ADR38586 standard; peptide; 15 AA. Human CD59 amino acids 36-50. 18-NOV-2004 (first entry) US2004166531-A1 Key Modified-site Homo sapiens 26-AUG-2004 ADR38586; ADR38586

08-MAY-2000; 2000US-0203254P. 16-APR-2001; 2001US-00835752. (HALP/) HALPERIN J.

Halperin J;

WPI; 2004-634394/61.

Determining impact of blood sugar level on glycation levels in diabetic patient involves measuring level of lysine residue at specific position in glycated membrane protein associated with regulation of complement system.

Example 5; SEQ ID NO 1; 18pp; English.

The invention relates to determining the impact of blood sugar level on protein glycation levels in a subject involves measuring a level of lysine residue at position 41 in a glycated membrane protein CD59 (K41-glycated CD59) from a sample (e.g. urine). Also included are evaluating/selecting a treatment for regulating blood sugar levels (e.g. in a patient suffering from diabetes mellitus), determining regression, progression or onset of a condition caused by abnormal levels of glycated protein, treating a subject to reduce the risk of or progression of

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Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;
autoimmune disease; inflammation; cancer; nervous system disease;
                                                                                                                                                       Human SNP related amino acid sequence SEQ ID NO:1248.
                                                                               ABB56683 standard; peptide; 14 AA.
                                                                                                                                                                                                                     infection; polymorphic protein.
                                                                                                                                                                                                                                                                                                                         22-NOV-2000; 2000WO-US032311.
                                                                                                                                 05-MAR-2002 (first entry)
 |||: |: ||
2 EHCSLNENTT 11
                                                                                                                                                                                                                                                                                                                                                                          (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                       WO200138586-A2.
                                                                                                                                                                                                                                                                                                                                                  24-NOV-1999;
                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                31-MAY-2001,
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Matches
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disorder associated with abnormally high levels of K41-glycated CD59, a Composition comprising isolated, pure or fragment of isolated K41-glycated CD59. The method is used to K41-glycated CD59 with not to K41-nonglycated CD59. The method is used to monitor glycaemic control in a diabetic patient, and to select subject for therapy, to monitor onset, progression and/or regression of diabetes or other diseases by monitoring levels of glycated CD59 in subject. The method provides direct indication of the level of the subject. S glycaemic control thus effectively CD59 can be detected in urine, thus obviating the need for a blood sugar levels or glycation levels. The glycated sample. The present sequence is a peptide used to raise anti-CD59 antibodies, comprising amino acids 36-50 of human CD59.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to use of a prosaposin-related peptide or derivative, in the production of a medicament for use in preventing or delaying cell death, or in promoting the expression of cell death supporting gene product Bol-XL. The invention is useful for preventing the death of cells e.g. brain cells, neurons and cardiac muscle cells, i
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of prosaposin-related peptides or derivatives as cytoprotective agents, for suppressing apoptosis or apoptosis-like cell death.
                                                                                                                                                                                                                        ö
                                                                                                                                                                                               8; Length 15;
                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      Prosaposin; cell death; Bcl-XL; brain; cardiac muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sadamoto
                                                                                                                                                                                             Score 43; DB 8
Pred. No. 8.6;
                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Morita F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 12; 41pp; English.
                                                                                                                                                                                                                                                                                                                                     AAB67300 standard; peptide; 16 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sato K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39.6%;
                                                                                                                                                                                             44.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-2000; 2000EP-00305504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99JP-00185155
                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                         Local Similarity 87.5 es 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tanaka J,
                                                                                                                                                                                                                                                                       7 FEHANFND 14
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                                                                                                                                                                                                                                                                                                                                                                                                                Cytokine peptide #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-204263/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SAKA/) SAKANAKA M.
(TANA/) TANAKA J.
                                                                                                                                                                                                                                              1 FEHCNFND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vitro or ex vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16 AA;
                                                                                                                                                                     Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SATO/) SATO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP1072609-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sakanaka M,
                                                                                                                                                                                                                                                                                                                                                                                       20-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                               AAB67300;
                                                                                                                                                                                             Query Match
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99US-0167383P

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comprising one or more single nuclectide polymorphisms (SDPS). ABB56531

Conjournelocides The sequences from the present invention can have clienteded. ABB56903 represent human peptides encoded by some of the SNP coligonucleotides. The sequences from the present invention can have immunosuppressive, cytostatic, antiinflammatory, neuroprotective and antimodiaes from the present invention can be used for treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism. The pathology may be autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. The SNPs are also useful for determining which forms of a characterised polymorphism are present in individuals. The antibodies may be used in the detection, quantitation and/or cellular or tissue localisation of a polymorphic protein (e.g., for use in measuring levels of the polymorphic protein within appropriate physiological samples)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                        Isolated human nucleic acids comprising one or more single nucleotide polymorphisms, useful for treating a subject suffering from a pathology, e.g. autoimmune diseases, ascribed to the presence of a sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     ABL00010 to ABL01104 represent human nucleic acid oligonucleotides
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Pred. No. 1e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADM33098 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 620; 674pp; English.
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50.0%;
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QHCSRNNFTMRL 14
Shimkets RA, Leach M;
                                                                  WPI; 2001-355949/37.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14 AA;
                                                                                                                                                                                                                                                             polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADM33098
ID ADM3
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Gaps

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2; Indels

DB 4; Length 16; 56;

Score 38; DB 4 Pred. No. 56; 2; Mismatches

Query Match Best Local Similarity 60.0 Matches 6; Conservative

EHCNFNDVTT 11

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Roush CL,

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New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
                                                                                                                                             (LIFE-) LIFESPAN BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                         Claim 1; Fig 2; 523pp; English.
                                                                                                                   19-DEC-2000; 2000US-0257144P
                                                                                         19-DEC-2001; 2001WO-US050107
                                                                                                                                                                                                                                                                autoimmune diseases.
                                                                                                                                                                                               WPI; 2003-046718/04
                                       WO200261087-A2
              Homo sapiens.
                                                                 08-AUG-2002
                                                                                                                                                                     Burmer GC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; G protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; call regeneration-related disease; ALDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzbeimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma; ulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TAT protein and HIV-1 gp120 which are useful for inhibiting the entry of HIV-1 into a host cell. The inhibitors of the interaction between HIV-1 TAT protein and HIV-1 gp120 are useful for inhibiting the entry of HIV-1 into a host cell for treating infections caused by M-tropic or L-tropic HIV-1 strains. This sequence represents a peptide derived from the HIV-1 TAT86 protein which is used as an inhibitor of HIV-1 entry into cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates to novel inhibitors of the interaction between HIV-
                                                                                                                                                                                                                                                                                                                                                      Use of inhibitors of the interaction between HIV-1 TAT protein and HIV-1 gpl20 for inhibiting the entry of HIV-1 into a host cell for treating infections caused by M-tropic or L-tropic HIV-1 strains.
                                                                                      TAT; gp120; HIV-1 cell entry inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1174
                                                             Human immunodeficiency virus 1 cell entry inhibitor peptide #126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33.5; DB 8; Length 15; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          Claim 21; SEQ ID NO 127; 87pp; English.
                                                                                                                                                                                                                                                                           (CREA-) CREABILIS THERAPEUTICS SRL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP82501 standard; peptide; 16 AA
                                                                                      anti-HIV; gene therapy; HIV-1; M-tropic HIV-1;
                                                                                                                              Human immunodeficiency virus 1
                                                                                                                                                                                                                                    13-SEP-2002; 2002EP-00020649.
19-DEC-2002; 2002EP-00028510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.9%;
50.0%;
                                                                                                                                                                                                           12-SEP-2003; 2003WO-EP010162
                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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CSFN-ITTEIRD 11
                                                                                                                                                                                                                                                                                                      Bussolino F, Marchio S;
                                                                                                                                                                                                                                                                                                                               WPI; 2004-269894/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                        WO2004024173-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15 AA;
                                      17-JUN-2004
                                                                                                                                                                                   25-MAR-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                     gp120
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The present interiors an assay for the detection of a particular or acids. Also described: (1) an assay for the detection of a particular or acids. Also described: (1) an assay for the detection of a particular or acids. Also described: (1) an assay for the detection of a particular G or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (1) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody squinst a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the gresence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, immunological-related ciseases, cell creating immune diseases, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, catheroscierosis, bacterial, fungal, protozoan or viral infections, other contral infections, other contral infections, catheroscierosis, cancer, cardiomyopathy, chronic and acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memoral sos, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode GPCR proteins given in ABPB1675 to ABPR82018, which are used in the exemplification of the present invention
    comprising: (a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Indels
present invention describes antigenic peptides (I)
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Pred. No. 3.5e+02;
2; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY58596 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNFNDVTTRLRENE 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.4
Best Local Similarity 42.9
Matches 6; Conservative
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ID AAYS
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Matches
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ADC17402
ID ADC1
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                                                                                                                                                                                                                                                                                               The invention relates to the recombinant production of the toxoplasma antigen SAG1 or a fragment thereof in the yeast Pichia pastoris. SAG1 is the major surface antigen of Toxoplasma gondii, an obligate intracellular protozoan parasite responsible for toxoplasmosis in mammals, including humans. SAG1 is anchored to the plasma membrane of T. gondii via a GPI (glycosyplpossphatidylinositol) anchor, which is atteched to the C-terminal anchor region (residues 308-336). The invention provides a truncated SAG1 protein, which lacks the anchor region and comprises amino acids 48-307, and a SAG protein N-terminally fused to a yeast secretion signal peptide. The SAG1 protein and its fragments can be used in the manufacture of a subunit vaccine for the prevention or treatment of toxoplasmosis in mammals. A live attenuated Toxoplasma vaccine is available, but cannot be administered to humans due to the risk of recombinant expression of SAG1 has been attempted in Escherichia coli,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mammalian cells or S. cerevisiae, but has been associated with problems such as misfolding and insolubility, low yields of correctly folded SAG1, or heterogeneous protein production. In addition, purification of the native protein from tachyzoites is difficult and time-consuming, due to the GPI anohor. Sequences AAY58595-Y55596 represent peptide epitopes of T. gondii SAG1, which were used to raise polyclonal antibodies in an exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ingrogness intributor; unsure growth inhibitor;
tumour metastasis inhibitor; tumour growth inhibitor;
endothelial cell interaction inhibitor;
basal lamina membrane formation inhibitor; cytostatic; antipsoriatic;
antianaemic; ophthalmological; antiarteriosclerotic; antiulcer;
endothelial cell adhesion inhibitor;
                                                                                                                                                                                                                                               Method for production of toxoplasma antigen SAG1 for use in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 33.9%; Score 32.5; DB 3; Length 16; Local Similarity 43.8%; Pred. No. 4.1e+02; les 7; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Type IV collagen NC1 domain related peptide SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           crystallised NC1 domain hexamer of type IV collagen; angiogenesis inhibitor; angiogenesis-mediated disease;
                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADC17406 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                         Example 1; Page 14; 47pp; English
                                                                                                                                                                                          Biemans R, Bollen A, Haumont M;
                                                                                                                      98GB-00012773.
                                                                                             99WO-EP003957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 CN---FNDVTTRLREN 16
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                                                                                                                                                                                                                  WPI; 2000-106101/09.
              Toxoplasma gondii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16 AA;
                                         WO9966043-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-DEC-2003
                                                                                             08-JUN-1999;
                                                                                                                      12-JUN-1998;
                                                                                                                                      15-APR-1999;
                                                                  23-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADC17406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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The present invention describes a crystallised NCI domain hexamer of type C IV collagen (I). Also described: (1) a chimeric polypeptide; (2) a pharmaceutical composition comprising the polypeptide and a carrier; (3) inhibiting angiogenesis in tissue; (4) treating an angiogenesis-mediated disease or condition in a mammal; (5) inhibiting tumour metastasis or growth; (5) inhibiting endothelial cell interaction with the extracellular matrix in an animal tissue; (6) inhibiting basal lamina membrane formation in cell or tissue; (6) inhibiting basal lamina comprane formation in cell or tissue; (6) inhibiting basal lamina membrane of type IV collagen; (8) identifying inhibitors of type IV collagen assembly; and (9) an inhibitor of type IV collagen assembly. A crystallised NCI domain hexamer of type IV collagen (I) has cytostatic, antianaemic, ophthalmological, antiarteriosclerotic and antiulora activities, and can be used as an inhibitor of angiogenesis, cumour growth, tumour metastasis, endothelial cell adhesion, endothelial cell proliferation, and basal lamina assembly. A (I) polypeptide can be used for treating of glaucoma, sickle cell anaemia, ulcerative colitis, cor for inhibiting bumour metastasis, cor for inhibiting bumour metastasis or growth, inhibiting endothelial coll sease or condition with the extracellular matrix in an animal tissue, and controllar and assembly. A (I) the cell or tissue cells intracation with the extracellular matrix in an animal tissue, and controllar and assembly.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptide, useful for treating an angiogenesis-mediated disease or condition consisting of glaucoma or blood-borne tumors or for inhibiting basal lamina membrane formation in cell or tissue development.
endothelial cell proliferation inhibitor; glaucoma; sickle cell anaemia; ulcerative colitis; psoriasis; atherosclerosis; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; SEQ ID NO 7; 168pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001US-0351289P.
2002US-0366854P.
                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUL-2002; 2002WO-US023763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001US-0308523P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sundaramoorthy M, Hudson B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUNDARAMOORTHY M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                 blood-borne tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUND/) SUNDARAMC
(HUDS/) HUDSON B.
                                                                                                                                                                                                                                                                                     WO2003012122-A2
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                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-OCT-2001;
22-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                          13-FEB-2003
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                                                                                                                                                               Synthetic.
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angiogenesis inhibitor; angiogenesis-mediated disease; tumour metastasis inhibitor; tumour growth inhibitor; endothelial cell interaction inhibitor; cytostatic; antipsoriatic; antianaemic; ophthalmological; antiarteriosclerotic; antiulcer; endothelial cell adhesion inhibitor; cytostatic; antiulcer; endothelial cell adhesion inhibitor; glaucoma; sickle cell anaem ulcerative colitis; psoriasis; atherosclerosis; rheumatoid arthritis;
                                  Type IV collagen NC1 domain related peptide SEQ ID NO:3.
                                                   crystallised NC1 domain hexamer of type IV collagen;
                                                                                                                                                                                                                                                                            (UNIV ) UNIV KANSAS MEDICAL CENT
                                                                                                                                                                                                                              27-JUL-2001; 2001US-0308523P.
29-OCT-2001; 2001US-0351289P.
22-MAR-2002; 2002US-0366854P.
                                                                                                                                                                                                              26-JUL-2002; 2002WO-US023763.
                                                                                                                                                                                                                                                            03-JUN-2002; 2002US-0385362P.
                 (first entry)
                                                                                                                                                                                                                                                                                      SUNDARAMOORTHY M
                                                                                                                                  olood-borne tumour.
                                                                                                                                                                                                                                                                                                                 Sundaramoorthy M,
                                                                                                                                                                                                                                                                                              (HUDSON B.
                                                                                                                                                                            WO2003012122-A2.
                                                                                                                                                           Homo sapiens.
                 18-DEC-2003
                                                                                                                                                                                              13-FEB-2003.
                                                                                                                                                 Synthetic.
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anaemia;

Hudson B;

WPI; 2003-332730/31.

New polypeptide, useful for treating an angiogenesis-mediated disease or condition consisting of glaucoma or blood-borne tumors or for inhibiting basal lamina membrane formation in cell or tissue development.

Claim 5; SEQ ID NO 3; 168pp; English.

Inhibiting angiogenesis, angiogenesis-mediated diseases or conditions, tumor metastasis, and tumor growth, involves contacting subject with crystallized type IV collagen NCI domain hexamer polypeptide.

Disclosure, SEQ ID NO 3; 178pp; English.

The present invention describes a crystallised NCI domain hexamer of type IV collagen (I). Also described: (1) a chimeric polypeptide and a carrier; (2) a chharmaceutical composition comprising the polypeptide and a carrier; (3) inhibiting angiogenesis in tissue; (4) treating an angiogenesis-mediated disease or condition in a mammal; (5) inhibiting tumour metastasis or extracellular matrix in an animal lissue; (6) inhibiting basal lamina membrane formation in cell or tissue development; (7) a crystal of an NCI contagen assembly, and (9) an inhibitor of type IV collagen assembly. A crystallised NCI domain hexamer of type IV collagen (I) has cytostatic, antipsoriatic, antiansemic, ophthalmological, antiateriosclerotic and antipsoriatic, antiansemic, ophthalmological, antiateriosclerotic and antiplocra activities, and can be used as an inhibitor of angiogenesis, tumour growth, tumour metastasis, endothelial cell adhesion, endothelial cell proliferation, and basal lamina assembly. A (I) polypeptide can be used for treating of glaucoma, sickle cell anaemia, ulcerative colitis, consisting of glaucoma, sickle cell anaemia, ulcerative colitis, consisting of glaucoma, sickle cell anaemia, ulcerative colitis, corsisting basal lamina membrane formation in cell or tissue cellopment. The methods are useful for inhibiting angiogenesis in tissue, inhibiting the are useful for inhibiting endothelial cell interaction with the extracellular matrix in an animal tissue, and cidentifying inhibitors of type IV collagen assembly. The present expresent invention

The invention relates to a novel method for inhibiting angiogenesis, and angiogenesis-mediated diseases or conditions, tumour metastasis, and tumour growth, involving contecting a subject with a crystalised type IV collagen NC1 domain hexamer polypeptide. A polypeptide of the invention has angiogenic, cutiathritic, immunosuppressive, antiseborrheic, antibacterial, vulnerary, antiulcer, fungicide, virucide, protozoacide, anti-HIV, antiinflammatory, antianaemic, antisickling, cateopathic, vasorropic, gastrointestinal, antipsoriatic, and of cateopathic, vasorropic, gastrointestinal, antipsoriatic, and of cateopathic, vasorropic, gastrointestinal, antipsoriatic, and of cateopathic, vasorropic, gastrointestinal, antipsoriatic, and catefaction antiatherosclerotic activity. The polypeptide inhibits assembly of type IV collagen heterotrimers and hexamers. The method of the invention is useful for inhibiting angiogenesis, angiogenesis-mediated diseases or conditions, tumour metastasis and tumour growth. The angiogenesis or conditions, thematorial angiogenesis, angiogenesis magiogenesis.

Tetinopathy of prematurity, corneal graft rejection, neovascularisation, mecular degeneration, corneal neovascularisation, mecular degeneration, corneal neovascularisation, chorolarial fibroplasia, epidemic keratoconjunctivitis, cyphyllis, Mycobacteria infections, lipid degeneration, chemical burns, cyphyllis, Mycobacteria infections, lappaes simplex infections, Harpes zoster infections, protozoan infections, Raposi's sarcoma, Mooren ulcer, Terrien's marginal degeneration, maginal keratolysis, trauma, systemic lupus, polyarteritis, Megeners sarcoidosis, scleritis, Steven's Johnson Lupus, polyarteritis, Regeners sarcoidosis, scleritis, scleven's Johnson

Sequence 14 AA;

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                                                                                                                                                                                        angiogenesis, angiogenesis-mediated disease, tumour metastasis, tumour growth, type IV collagen, NC1 domain hexamer; angiogenic; cytostatic; antidiabetic; ophthalmological, antirheumatic; antiarthritic; immunosuppressive, antiseborrheic; dermatological, antibacterial; vulnerary; antiulcer; fungicide; virucide; protozoacide; anti-HIV; antiinflammatory; antianaemic; antistckling; osteopathic; vasotropic; gastrointestinal; antipsoriatic; antiatherosclerotic.
                            Gaps
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                                                                                                                                                                      Human type IV collagen NC1 inter-CDSR alpha3 chain peptide.
         Score 32; DB 7; Length 14; Pred. No. 4.3e+02; Mismatches 3; Indels
                                                                                                                ADR18924 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                   (UNIV ) UNIV KANSAS MEDICAL CENT.
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                                                                                                                                                     04-NOV-2004 (first entry)
Query Match
Best Local Similarity 60...
6; Conservative
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                                                                FLFCNVNDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 angiogenesis; angiogenesis-mediated disease; tumour metastasis; tumour growth; type IV collagen; NC1 domain hexamer; angiogenic; cytostatic; antidiabetic; ophthalmological; antirheumatic; antiarthritic; immunosuppressive; antiseborrheic; dermatological; antibacterial; vulnerary; antiulcer; fungicide; virucide; protozoacide; anti-HIV; antinflammatory; antianaemic; antisickling; osteopathic; vasotropic; gastrointestinal; antipsoriatic; antiatherosclerotic.
disease, radial keratotomy, sickle cell anaemia, sarcoid, pseudoxanthoma elasticum, Paget's disease, vein occlusion, artery occulsion, carctid obstructive disease, chronic uveitis, chronic vitritis, Lyme's disease, pars glanditis, tyme's disease, myopia, optic pits, Stargarts disease, toxoplasmosis, post-laser complications, abnormal proliferation of fibrovascular tissue, haemangiomas, Osler Weber-Rendu, AIDS, occular neovascular disease, osteoarthritis, chronic inflammation, Crohn's fibrase, ulcerative colitis, psoriasis, atherosciarosis and pemphigoid. The present sequence represents a peptide of the invention, derived from type IV collagen crystallised NCI domain hexamer.
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                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumor metastasis, and tumor growth, involves contacting subject with
crystallized type IV collagen NC1 domain hexamer polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human type IV collagen NC1 inter-CDSR alpha6 chain peptide.
                                                                                                                                                                                                                                                                                                        33.3%; Score 32; DB 8; Length 14; 66.7%; Pred. No. 4.3e+02; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 7; 178pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADR18928 standard; peptide; 14 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-JAN-2003; 2003US-0443133P.
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                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         FLFCNVNDV 10
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                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 6: Conger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2004067762-A2.
                                                                                                                                                                                                                                                                  Sequence 14 AA;
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                                                                                                                                                 plaucoma, retrolental fibroplasia, epidemic keratoconjunctivitis, preringarum, retrolental fibroplasia, epidemic keratoconjunctivitis, prerygium keratitis sica, sjogren's, acne rosacea, phylactenulosis, syphilis, mycobacteria infections, lipid degeneration, chemical burns, infections, protozoan infections, Raposi's sarcoma, Mooren ulcer, infections, protozoan infections, Raposi's sarcoma, Mooren ulcer, infections, protozoan infections, Raposi's sarcoma, Mooren ulcer, lupus, polyarteritis, Wegeners sarcoldosis, scleritis, Steven's Johnson disease, radial keratotomy, sickle cell anaemia, sarcoid, pseudoxanthoma elasticum, Paget's disease, vein occlusion, artery occulsion, carotid obstructive disease, chronic uveitis, chronic vitritis, Lyme's disease, bales disease, myopia, optic pits, Stargarts disease, pars planitis, chronic retinal detachment, hyperviscosity syndromes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR83791 is an amino-terminal peptide of a virus infection factor derived
from heat-treated silkworm body fluid. The new virus infection factor
IV collagen heterotrimers and hexamers. The method of the invention is useful for inhibiting angiogenesis, angiogenesis-mediated diseases or conditions, tumour metastasis and tumour growth. The angiogenesis-mediated disease or condition is solid and blood-borne tumours, diabetic retinopathy, rheumatoid arthritis, retinal neovascularisation, choroidal neovascularisation, macular degeneration, corneal neovascularisation, retinopathy of prematurity, corneal graft rejection, neovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino terminal; silkworm; virus infection factor; promoter; recombinant;
                                                                                                                                                                                                                                                                                                                                                                                                                   toxoplasmosis, post-laser complications, abnormal proliferation of fibrovascular tissue, haemangiomas, Osler Weber-Rendu, AIDS, ocular neovascular disease, osteoarthritis, chronic inflammation, Crohn's disease, ulcerative colitis, psoriasis, atherosclerosis and pemphigoid. The present sequence represents a peptide of the invention, derived fro type IV collagen crystallised NC1 domain hexamer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virus infection factor from silkworm body fluid - used to promote infection of insect cells with protein-expressing recombinant virus in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virus infection factor N-terminal peptide from silkworm body fluid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.3%; Score 32; DB 8; Length 14; 55.6%; Pred. No. 4.3e+02; Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR83971 standard; peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Conservative
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FIYCNINEV 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-371176/48.
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                culture medium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-NOV-1994;
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21-MAY-1996
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New modified human erythropoietin molecules with reduced immunogenicity, useful in various therapeutic applications such as in the treatment of
                                                                                                                                 erythropoietin; EPO; non-immunogenic; immunogenic; EPO manufacture; erythropoietin manufacture; anaemia; human.
                                                                                                        Human erythropoietin (BPO) protein-related epitope peptide #44.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 25; 38pp; English.
                            ADK70612 standard; peptide; 15 AA
                                                                                                                                                                                                                                                                            09-AUG-2002; 2002EP-00017914.
                                                                                                                                                                                                                                                   07-AUG-2003; 2003WO-EP008725.
                                                                                                                                                                                                                                                                                                     (MERE ) MERCK PATENT GMBH.
                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-226801/21.
                                                                                                                                                                                                                                                                                                                                Carr FJ;
                                                                                                                                                                                                 WO2004018515-A2
                                                                                                                                                                        Homo sapiens
                                                                               20-MAY-2004
                                                                                                                                                                                                                         04-MAR-2004
                                                    ADK70612;
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                                                                                                                                                                                                                                                                                                                                                                                                             anemia.
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  RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention relates to a novel modified molecule comprising the biological activity of human erythropoietin (BPO) and being substantially non-immunogenic or less immunogenic than any non-modified molecule having the same biological activity in an individual when used in vivo. The invention is useful for manufacturing a modified human erythropoietin amplications, such as in the treatment of anaemia. The present sequence is that of a human EPO epitope peptide which is related to the invention.
(VIF) is useful for promoting the infection of insect cells with recombinant nuclear polyhedrosis virus. The virus having been recombined with a useful protein-expressing gene. The insect cell can then be cultured and the useful protein expressed at high yields. The new VIF has a mol. wt. of approx. 15.2 kba and an isoelectric point of 9 or higher. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New modified human erythropoietin molecules with reduced immunogenicity, useful in various therapeutic applications such as in the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                           Human erythropoietin (EPO) protein-related epitope peptide #45.
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                                                                                                                                             1; Indels
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Pred. No. 4.7e+02;
2; Mismatches 3;
                                                                                                                  Score 32; DB 2; I Pred. No. 4.7e+02; 0; Mismatches 1;
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                                                                                                                                                                                                                                                               ADK70613 standard; peptide; 15 AA.
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                                                                                                                    33.3%;
87.5%;
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                                                                                                                                Similarity 87.5
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Best Local Similarity
5; Conserve
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FNVVTTRL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carr FJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2004018515-A2.
                                                                                           Sequence 15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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This invention relates to a novel modified molecule comprising the biological activity of human erythropoietin (EPO) and being substantially non-immunogenic or less immunogenic than any non-modified molecule having the same biological activity in an individual when used in vivo. The invention is useful for manufacturing a modified human erythropoietin molecule. The modified BPO may be used in various therapeutic applications, such as in the treatment of anamnia. The presence is that of a human EPO epitope peptide which is related to the invention.
                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                    Score 32; DB 8; Length 15; Pred. No. 4.7e+02; 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADK70576 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                      33.3%;
50.0%;
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EHCSLNENIT 13
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Matches 5; Conserv
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EHCNFNDVTT

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                                                                                                                                               New modified human erythropoietin molecules with reduced immunogenicity, useful in various therapeutic applications such as in the treatment of
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                                                                                                                                                                                                       Disclosure; Page 15; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADK70658 standard; peptide; 15 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 27; 38pp; English
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              07-AUG-2003; 2003WO-EP008725.
                                        09-AUG-2002; 2002EP-00017914
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                                                                (MERE ) MERCK PATENT GMBH
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                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                           Baker M, Carr FJ;
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This invention relates to a novel modified molecule comprising the

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non-immunogenic or less immunogenic than any non-modified molecule having the same biological activity in an individual when used in vivo. The invention is useful for manufacturing a modified human exythropoietin molecule. The modified EPO may be used in various therapeutic applications, such as in the treatment of anaemia. The present sequence is that of a human EPO epitope peptide which is related to the invention.
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biological activity of human erythropoietin (EPO) and being substantially
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Pred. No. 4.7e+02;
2; Mismatches 3; Indel8
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4 EHCSLNENIT
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Best Local Similarity
Matches 5; Conserv
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Sequence 3, Appli Sequence 7, Appli Sequence 3, Appli Sequence 16, Appl Sequence 123, App Sequence 1294, Ap Sequence 1594, Ap

Sequence 1597, Ap Sequence 1597, Ap Sequence 298, App

Sequence 1, Ap Sequence 1597

Sequence 11, Appl Sequence 20, Appl Sequence 22, Appl Sequence 23, Appl Sequence 20, App Sequence 28, Appl Sequence 4, Appl Sequence 38, Appl Sequence 38, Appl Sequence 35, Appl Sequence 35, Appl Sequence 39, Appl Sequence 23, Appl

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Searched:

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Sequence 4, Application US/10870342A
Publication No. US20050032128A1
GENERAL INFORMATION:
APPLICANT: Halperin, Jose
TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
FILE REFERENCE: H0498.70223US00
CURRENT APPLICATION NUMBER: US/10/870,342A
CURRENT FILING DATE: 2004-06-17
NUMBER OF SEQ ID NOS: 49
SOTID NO 4
SEQ ID NO 4
SEQ ID NO 4
SEQ ID NO 5
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US-10-670-342A-16
US-10-670-342A-16
; Sequence 16, Application US/10870342A
; Fublication No. US20050032128A1
; GENERAL INFORMATION:
; APPLICAWT: Halperin, Jose
; TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.2%; Score 52; DB 17; Length 13; 100.0%; Pred. No. 0.14; ive 0; Mismatches 0; Indels
4 US-10-206-699-3

4 US-10-206-699-7

6 US-10-46-442-16

US-09-999-919-123

US-09-999-919-123

US-00-999-919-123

US-10-395-032-1594

US-10-395-032-1594

US-10-395-032-1597

US-10-395-032-1597

US-10-395-032-119

US-10-306-699-301

US-10-206-699-301

US-10-206-699-301

US-10-206-699-4

US-10-462-262-202

US-10-462-262-202

US-10-462-262-303

US-10-462-262-303

US-10-462-315-260/37

US-10-462-262-303

US-10-462-315-260/37

US-10-482-115-260/37

US-10-482-115-260/37

US-10-482-115-260/37

US-10-147-910-35

US-10-162-115-260/37

US-10-162-115-260/37

US-10-162-111

US-10-162-111

US-10-163-111

US-10-203-423-182

US-10-486-333-182

US-10-468-543-12
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Best Local Similarity 100.
Matches 8; Conservative
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Sequence 3, Appli
Sequence 10, Appli
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Sequence 1, Appli
Sequence 21, Appli
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Sequence 23,
Sequence 3, A
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43.445 Million cell updates/sec
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Sequence 124
Sequence 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Applications AA:*

| cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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| cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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                                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-870-342A-16
US-10-870-342A-3
US-10-870-342A-3
US-10-870-342A-10
US-10-870-342A-10
US-10-873-581-1
US-10-870-342A-17
US-10-870-342A-17
US-10-870-342A-17
US-10-870-342A-17
US-10-870-342A-17
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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seq length: 17
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Result Š. 2244444446

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US-10-870-342A-23
US-10-870-342A-23
Sequence 23, Application US/10870342A
Publication No. US20050032128A1
GENERAL INFORMATION:
APPLICANT: Halperin, Jose
TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
FILE REFERENCE: H0498.70223US00
CURRENT APPLICATION NUMBER: US/10/870,342A
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PATENTING DATE: 2004-06-17
NUMBER OF SEQ ID NOS: 49
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Publication No. US20050032128A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/870,342A
CURRENT FILING DATE: 2004-06-17
UNMBER OF SEQ ID NOS: 49
SOFTWARE: PATENTIN VEXSION 3.2
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44.8%; Score 43; DB 17; Length 14;
Best Local Similarity 87.5%; Pred. No. 4.3;
Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                       DB 17; Length 16; 0.18;
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FILE REFERENCE: H0498.70223US00
CURRENT PEPLICATION NUMBER: US/10/870,342A
CURRENT FILING DATE: 2004-06-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin version 3.2
SEQ ID NO 16
LENGTH: 16
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Best Local Similarity 100..
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Best Local Similarity 87.5
....hes 7; Conservative
                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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US-10-870-342A-3
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LENGTH: 14
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LENGTH: 14
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US-09-835-752-1
Sequence 1, Application US/09835752
Sequence 1, Application WOS/09835752
Publication No. US20040166531A1
GENERAL INFORMATION:
APPLICANT: Halperin. Jose
TITLE OF INVENTION: Methods, Products and Treatments for Diabetes
FILE REFERENCE: H0498/7137(ERG)
CURRENT APPLICATION WINBER: US 08/09/835,752
CURRENT PLING DATE: 2001-04-16
PRIOR APPLICATION WUMBER: US 06/203,254
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
                                                                                                                                                                                APPLICANT: Halperin, Jose
TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
FILE REFERENCE: H0498.7022301850
CURRENT APPLICATION NUMBER: US/10/870,342A
CURRENT FILING DATE: 2004-06-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin version 3.2
SEQ ID NO 10
LENGTH: 14
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US-10-833-581-1
US-10-833-581-1
; Sequence 1, Application US/10833581
; Publication No. US20040219606A1
; GENERAL INFORMATION:
; APPLICANT: Halperin, Jose
; TILLE OF INVENTION: Methods, Products and Treatments for Diabetes;
; FILE REFERENCE: H0498/137(ERG)
; CURRENT APPLICATION NUMBER: US/10/833,581
; CURRENT FILING DATE: 2004-04-28
; PRIOR FILING DATE: 2001-04-16
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Best Local Similarity 87.5%;
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Best Local Similarity 87.5
Matches 7; Conservative
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ORGANISM: Homo sapiens
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6 FEHANFND 13
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                                                                       RESULT 5
US-10-870-342A-10
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JS-10-813-638-1248
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US-10-206-699-3
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US-10-870-342A-21
Sequence 21, Application US/10870342A
Fublication No. US20050032128A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ANTI-GLYCATED CDS9 ANTIBODIES AND USES THEREOF
TITLE REFERENCE: H0498.70223US00
CURRENT APPLICATION NUMBER: US/10/870,342A
CURRENT FILING DATE: 2004-06-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin version 3.2
SEQ ID NO 21
LENGTH: 13
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TITLE OF INVENTION: ANTI-GLYCATED CD59 ANTIBODIES AND USES THEREOF
FILE REFERENCE: H0498.70223US00
CURRENT APPLICATION NUMBER: US/10/870,342A
CURRENT FILING DATE: 2004-06-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                          44.8%; Score 43; DB 16; Length 15; 87.5%; Pred. No. 4.7; cive 0; Mismatches 1; Indels
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41.7%; Score 40; DB 17; Length 13;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: US 06/203,254
PRIOR FILING DATE: 2000-05-08
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 15
TYPE: PRT
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Best Local Similarity 87.5-
اتامم 7; Conservative
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Best Local Similarity 100.
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ORGANISM: Homo sapiens
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FEHCNF 13
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US-10-870-342A-17
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LENGTH: 17
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Sequence-1248, Application US/10813638

Publication No. US20040235026A1

Publication No. US20040235026A1

Publication No. US20040235026A1

APPLICANT: Shiwkets, Richard A. APPLICANT: Shiwkets, Richard A. APPLICANT: Leach, Martin D. TITLE OF INVENTION: USE THEREOF TITLE OF INVENTION: USE THEREOF FILE REPERENCE: 15966-559

CURRENT APPLICATION NUMBER: US/10/813,638

CURRENT PILING DATE: 2004-03-29

PRIOR PILING DATE: 1999-11-24

NUMBER OF SEQ ID NOS: 1468

SOFTWARE: CuraGen Patent Formatter Version 0.9

SEQ ID NO 1248

LENGTH: 14
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APPLICANT: Brown, Joseph P.
APPLICANT: Roush, Christine C.
APPLICANT: Roush, Christine L.
APPLICANT: Roush, Christine L.
APPLICANT: Roush, Christine L.
APPLICANT: ROUSH, Christine L.
TITLE OF INVENTION: ANTICENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT PILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
SEQ ID NO 1174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 1174, Application US/10225567A; Publication No. US20030113798A1; GENERAL INFORMATION:
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CTHER INFORMATION: cSNP translation
US-10-813-638-1248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 CNFNDVTTRLRENE 17
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Best Local Similarity 50.0
Matches 6; Conservative
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TITLE OF INVENTION: Use of erythropoietin and erythropoietin mentics for the TITLE OF INVENTION: treatment of neuropathic pain FILE REFERENCE: 6627-PA1090 CURRENT APPLICATION NUMBER: US/10/455,697 CURRENT FILING DATE: 2003-06-05 PRIOR PRILING DATE: 2002-06-05 NUMBER OF SEQ ID NOS: 3 SOFTWARE: Patentin version 3.2 LENGTH: 16
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US-10-746-442-16
is Sequence 16, Application US/10746442
is Publication No. US20040121958A1
is GENERAL INFORMATION:
is APPLICANT: O'BEIGN. John S.
is TITLE OF INVENTION: METHODS FOR ALLEVIATING NEUROPATHIC PAIN
FILLE REFERENCE: 07256/024001
is CURRENT FILING DATE: 2003-12-24
is PRIOR APPLICATION NUMBER: US/10/746,442
is PRIOR FILING DATE: FILING DATE: 1997-09-11
is PRIOR FILING DATE: FILING DATE: 1997-09-11
is PRIOR FILING DATE: FILING DATE: 1996-03-05
is NUMBER OF SEQ ID NOS: 25
is SOFTWARE: PATENTING DATE: 1996-03-05
is SOFTWARE: PATENTING DATE: 1200-03-05
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Pred. No. 3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: modified human sequence US-10-455-697-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8, 2005, 11:21:20
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50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 50.0
Matches 5; Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
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2 EHCSLNENIT 11
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ORGANISM: Artificial
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Job time : 152 secs
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APPLICANT: Hudson, B.

APPLICANT: Hudson, B.

TILE OF INVENTION: Crystallized structure of Type IV Collagen NC1 Domain Hexamer:
FILE REPERENCE: MBHB 01-1017

CURRENT APPLICATION NUMBER: US 10/206,699

CURRENT FILING DATE: 2002-07-26

PRIOR APPLICATION NUMBER: US 60/368,523

PRIOR APPLICATION NUMBER: US 60/351,289

PRIOR FILING DATE: 2001-10-29

PRIOR FILING DATE: 2002-03-22

PRIOR FILING DATE: 2002-03-22

PRIOR FILING DATE: 2002-06-03

PRIOR FILING DATE: 2002-06-03

NUMBER OF SEQ ID NOS: 307

SOFTWARRE: Patentin Version 3.1

SOFTWARRE: Patentin Version 3.1
APPLICANT: Hudson, B.
TITLE OF INVENTION: CYStallized structure of Type IV Collagen NC1 Domain Hexamer
FILE REFERENCE: MBHB 01-1017
CURRENT APPLICATION NUMBER: US/10/206,699
CURRENT FILING DATE: 2002-07-26
FRIOR APPLICATION NUMBER: US 60/308,523
FRIOR PAPLICATION NUMBER: US 60/308,523
FRIOR PRING DATE: 2001-07-27
FRIOR PELING DATE: 2001-10-29
FRIOR PELING DATE: 2002-03-22
FRIOR PELING DATE: 2002-06-33
FRIOR FILING DATE: 2002-06-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.3%; Score 32; DB 14; Length 14; 66.7%; Pred. No. 2.6e+02;
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GENERAL INFORMATION; APPLICANT: Campana, Wendy Marie; APPLICANT: Myers, Robert R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 55.6
Matches 5; Conservative
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FIYCNINEV 10
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Matches 6; Conserv
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US-10-455-697-3
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US-10-206-699-7
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Sequence 23, Appl
Batent No. 5444158
Patent No. 5444158
Sequence 4, Appli
Sequence 6, Appli
Sequence 12, Appl
Sequence 16, Appl
Sequence 1
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Sequence 11, Appl
Sequence 16, Appl
Sequence 1594, Ap
Sequence 1594, Ap
Sequence 1597, Ap
Sequence 2197, Ap
Sequence 21, Appl
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                                                                                                                                                                                     (without alignments)
30.215 Million cell updates/sec
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                                                                                                                                                         June 8, 2005, 10:59:08; Search time 42 Seconds
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/cgn2_6/ptoGata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptoGata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptoGata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptoGata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptoGata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-232-513A-11

US-09-231-159-16

US-08-611-307-16

US-09-187-859-1594

US-09-187-859-1594

US-09-187-859-1597

US-09-187-859-1597

US-09-758-621-21

US-09-107-858-21

US-09-107-858-21

US-09-579-174-21

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US-08-460-309-23

US-08-460-309-23
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US-08-908-3718-4

US-08-522-326-6

US-08-556-597-133

US-08-685-3578-12

US-08-95-2568-20

US-09-532-709G-1
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96
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                                                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 17
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Match
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                                                                                                                                                                                                                                                                                                                          Sequence:
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2 EHCNFNDVTT
                  TYPE: amino acid
                                ; TOPOLOGY: linear
US-09-231-159-16
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GY: linear
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Best Local Similarity
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US-08-611-307-16
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Patent No. 6268347
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Methods of Alleviating Neuropathic Pain
TITLE OF INVENTION: Using Prosaposin-Derived Peptides
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB 1; Length 17;
Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

SUFTWARE: PAPLICATION DATA:

APPLICATION NUMBER: US/09/231,159

FILING DATE:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/231,159

FILING DATE:

CURRENT APPLICATION OF PAR-1996

ATTORNEY AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REFERENCE/DOCKET NUMBER: P-UD 1928

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                           APPLICATION NUMBER: US/08/232,513A
FILING DATE: 21-APR-1994
GLASSIFICATION NUMBER: US/08/232,513A
FILING DATE: 21-APR-1994
APPLICATION NUMBER: US 08/100,247
FILING DATE: 30-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-UD 1643
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-901
21-APR-1994
0N: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: Peptide
LOCATION: 1..17
; CTHER INFORMATION: /label= hEPO
US-08-232-513A-11
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50.0%;
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Best Local Similarity 50.0.
Best Local Similarity 50.0.
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             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
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EHCSLNENIT 11
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STATE: California
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US-09-231-159-16
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APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
TITLE OF INVENTION: COMPONDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: COMPONDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REPERENCE: 1000686.407C;
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
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                                                                                                                                                                                                                                      Score 32; DB 3; Length 17; Pred. No. 74; 3; Indels 2; Mismatches 3; Indels
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ZOMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/611,307
FILING DATE: 05-MAR-1996
CLASSIFICATION NUMBER: US/08/611,307
FILING DATE: 05-MAR-1996
ATTONREY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REGISTRATION NUMBER: 31,815
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
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8.09-187-859-1594
; Sequence 1594, Application US/09187859A
; Patent No. 6358920
    33.3%;
50.0%;
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50.0%;
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    33.3
Best Local Similarity 50.0
Matches 5; Conservative
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2 EHCSLNENIT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: San Diego
STATE: California
COUNTRY: USA
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Gaps

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Sequence 1597, Application US/09839542B
; Sequence 1597, Application US/09839542B
; Ratent No. 656996
; GENERAL INFORMATION:
    APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CACHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT PILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21, Application US/08758621
Patent No. 5846821
GENERAL INFORMATION:
APPLICANT: Guerinot, Mary Lou, and Eide, David J.
TITLE OF INVENTION: Metal-Regulated Transporters and Uses Therefor CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Representative cyclic modulating agent based on CTHER INFORMATION: cadherin-8 cell adhesion recognition sequence US-09-839-542B-1597
  ; OTHER INFORMATION: cadherin-8 cell adhesion recognition sequence US-09-187-859-1597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31.2%; Score 30; DB 4; Length 9; 71.4%; Pred. No. 4.1e+05; ive 0; Mismatches 2; Indels
                                                                          Score 30; DB 3; Length 9;
Pred. No. 4.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,621
                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/018,578
FILING DATE: 29-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Silveri, Jean M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            & COCKFIELD
                                                                     n
Similarity 71.4%;
5; Conservative 0
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: LAHIVE & COC STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 31.2
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boston
STATE: Massachusetts
                                                                                                                                                                            4 CNFNDVT 10
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                                                                        Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                RESULT 8
US-09-839-542B-1597
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Sequence 1594, Application US/09839542B

Patent No. 656996

GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFRENCE: 100066.407D1
CURRENT APPLICATION NUMBER: US/09/839,542B
CURRENT APPLICATION NUMBER: US/09/839,542B
CURRENT FILING DATE: 2001.04-20
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 1594
LENGTH: B
                                                                                                                                                                                                                                                                                                                            Gaps
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Patent No. 6358920
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHENIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052.
                                                                                                                                                                          ; OTHER INFORMATION: Representative cyclic modulating agent based on ; OTHER INFORMATION: cadherin-8 cell adhesion recognition sequence US-09-187-859-1594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Representative cyclic modulating agent based on CTHER INFORMATION: cadherin-8 cell adhesion recognition sequence US-09-839-542B-1594
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                                                                                                                                                                                                                                                       Query Match 31.2%; Score 30; DB 3; Length 8; Best Local Similarity 71.4%; Pred. No. 4.1e+65; Matches 5; Conservative 0; Mismatches
                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1594
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Best Local Similarity 71.9.
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US-09-839-542B-1594
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US-09-187-859-1597
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LENGTH: 9
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Length 16;

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RESULT 14
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Fatent No. 6590140

FABERAL INFORMATION:

APPLICANT: GUARTION:

TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR

TITLE REFRENCE: DCI-099CPDV

CURRENT APPLICATION NUMBER: US/09/579,174

CURRENT FILING DATE: 1998-06-30

FRIOR APPLICATION NUMBER: 09/107,858

FRIOR FILING DATE: 1998-06-30

FRIOR FILING DATE: 1998-06-30

FRIOR FILING DATE: 1996-11-27

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PATENTIN VET. 2.0

SEQ ID NO 21

LENGTH: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Guerinot, Mary Lou et al.
APPLICANT: Guerinot, Mary Lou et al.
TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR FILE REFERENCE: DOIL-0990EDV
CURRENT APPLICATION NUMBER: US/09/107,858
CURRENT FILING DATE: 1988-06-30
EARLIER PILING DATE: 1996-11-27
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.2%; Score 30; DB 3; Length 16; 45.5%; Pred. No. 1.5e+02; tive 4; Mismatches 2; Indels
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: DCI-099CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-09-107-858-21
; Sequence 21, Application US/09107858
; Patent No. 6162900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: Arabidopsis thaliana
US-09-107-858-21
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ORGANISM: Arabidopsis thaliana
                                                                                                                                                     LENGTH: 16 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 45.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                              MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                   7 NDVTTRLRENE 17
                                                                                                                                                                                                                                                                                                                                                                                                           3 NDVTLPIKEDD 13
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Best Local Similarity
                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                         US-08-758-621-21
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Pred. No. 1.4e+02;
2; Mismatches 2; Indels
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                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
549652-8
; Patent No. 5496552
; Patent No. 5496552
; APPLICATION COSTEGENIC DEVICES
NUMBER OF ENCURION: OFFICATION DATA:
APPLICATION DATA:
TILING DATE: 29-JUN-1994
; PRIOR APPLICATION DATA:
APPLICATION NUMBER: 103,604
; PLING DATE: 06-AUG-1993
; APPLICATION NUMBER: 827,652
; FILING DATE: 28-JAN-1992
; FILING DATE: 28-JAN-1992
; FILING DATE: 28-JAN-1992
; FILING DATE: 07-SEP-1990
; FILING DATE: 08-APR-1998
; FILING DATE: 08-APR-1998
                                                                                                                                                    RESULT 12
5496552-8
; PATENT NO. 5496552
; PATENT NUMBERSABMPATH, THANGAVEL; RUEGER, DAVID C.
TITLE OF INVENTION:OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 25
; CUMERNT APPLICATION DATA:
APPLICATION NUMBER: US/08/268,252
FILING DATE: 29-UNN-1994
; PRICR APPLICATION NUMBER: 103,604
FILING DATE: 06-AUG-1993
APPLICATION NUMBER: 827,052
; FILING DATE: 28-UAN-1992
; APPLICATION NUMBER: 879,665
FILING DATE: 07-SEP-1990
; FILING DATE: 08-APR-1988
Score 30; DB 4; Pred. No. 1.5e+02;
                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.2%;
50.0%;
Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
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Best Local Similarity 50.0
Matches 4; Conservative
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                                                                     7 NDVTTRLRENE 17
                                                                                           3 NDVTLPIKEDD 13
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Matches 4; Conserv
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FLHCQFSE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO:8:
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Score 29; DB 2; Length 14; Pred. No. 1.9e+02;
                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,077
FILING DATE: 22-SEP-1993
CLASSIFICATION TATA:
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
PRIOR APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REFERENCE/DOCKET NUMBER: PLA 9721
TELEPAN: (619) 535-9001
TELEPAN: (619) 535-9001
TELEPAN: (619) 535-9001
TELEPAN: (619) 535-9001
TELEPAN: (19 0000 23: SEQUENCE CHARACTERISTICS: LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: June 8, 2005, 11:09:42 Job time: 43 secs
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Best Local Similarity 38.5.
Best Local Similarity 5.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 CNFNDVTTRLREN 16
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    San Diego
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
                                                                      92122
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Batent No. 5872231 5840863

GENERAL INFORMATION:
APPLICANT: Engvall, Eva
APPLICANT: Leivo, Ilmo
TITLE OF INVENTION: Pragments and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
                Sequence 23, Application US/08460309
Patent No. 5837496
GENERAL INFORMATION:
APPLICANT: Engvall, Eva
APPLICANT: Leivo, Ilmo
TITLE OF INVENTION: Fragments and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: Cambell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 14;
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CUNTER: USA

CUNTER: USA

CIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURSENTATION NUMBER: US/08/460,309

FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/125,077

FILING DATE: 22-28P-1994

PRICH APPLICATION NUMBER: US PCT/US 94/10730

FILING DATE: 21-SEP-1994

PRICH APPLICATION NUMBER: US 07/472,319

FILING DATE: 3-5AP-1996

PRICH APPLICATION DATA:
APPLICATION NUMBER: US 07/472,319

FILING DATE: 30-JAN-1990

PRICH APPLICATION DATA:
APPLICATION NUMBER: US 07/919,951

FILING DATE: 30-JAN-1990

RION APPLICATION NUMBER: US 07/919,951

FILING DATE: 30-JAN-1990

RATORNEY/AGENT INFORMATION:
NAME: CAMPADELL, 1992

ATTORNEY/AGENT NUMBER: P-LA 9721

TELECOMMUNICATION NUMBER: P-LA 9721

TELECOMMUNICATION NUMBER: P-LA 9721

TELECOMMUNICATION NUMBER: P-LA 9721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 29; DB 2; I Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 23
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.2%;
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                                                                                                                                                                                                                                                         STREET: 4370 La Jo
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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US-08-460-309-23
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Gaps ö

6; Indels

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Wed Jun

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

8, 2005, 10:32:41 ; Search time 29.6279 Seconds June Run on:

(without alignments)
84.435 Million cell updates/sec

US-09-020-393B-14_COPY_26_51

140 1 CLGYHLDVSLAFSEISVGAEFNKDDC 26 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Query Match Length DB	DB	ID	Descr
				;		
1	140	100.0		Н	C9HU	compl
7	52	37.1	n	~	T37964	proba
٣	49	35.0		~	PN0494	NAD A
4	49	35.0	524	7	A29677	compl
Ŋ	48	34.3		8	AG1117	trans
9	48	34.3		~	A11477	trans
7	48	34.3		7	AF0815	trans
80	46	32.9		~	T30493	hypot
Q	46	32.9	254	~	E84826	hypot
10	46	32.9		7	C70421	conse
11	46	32.9		7	JX0368	inter
12	46	32.9		7	T25933	hypot
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	Description	complement C9 prec	probable ubiquitin	NAD ADP-ribosyltra	complement C9 prec		transketolase homo	w	hypothetical prote	hypothetical prote	conserved hypothet	inter-alpha-trypsi	hypothetical prote	hypothetical prote	topoisomerase IV s	w.	hypothetical 39.2K	hypothetical prote	_	. hypothetical prote	hypothetical prote	н	ATP-dependent deox	fructokinases homo	fructokinases homo	hypothetical prote	hypothetical prote	4	ical	pyruvate dehydroge
SUMMARIES	ID	СЭНО	T37964	PN0494	A29677	AG1117	AI1477	AF0815	T30493	E84826	C70421	JX0368	T25933	T21712	C81822	D81055	JQ2174	S27909	C84265	T18567	T49010	T30319	AC1728	AE1176	AI1533	T18649	T19226	C88364	443	F81094
	DB	-	~	~	~	7	7	7	~	7	7	~	7	~	7	7	7	7	7	~	~	~	~	~	~	~	~	7	~	7
	& Query Match Length	:	3227	135	524	665	999	999	203	254	292	930	1372	2144	661	661	357	357	440	732	895	1189	1235	290	290	884	1002	1028	358	535
d	Query Match	100.0	37.1	35.0	35.0	4	34.3	34.3	32.9	32.9	32.9	32.9	32.9	32.9	32.5	32.5	32.1	32.1	32.1	32.1	32.1	32.1	32.1	31.8	31.8	31.8	ä	31.8	31.4	31.4
	Score		52	49	49	48	48	48	46	46	46	46	46	46	45.5	45.5	45	45	45	45	45	45	45	44.5	4.	4	•	4.	44	44
	ilt No.	1	7	ю	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22		24				28	53

dihydrolipoamide S	KRE11 protein - ye	transketolase NMB1	transketolase (EC	transketolase [imp	coagulation factor	transketolase [imp	probable cytoplasm	transketolase (EC	probable membrane	hypothetical prote	centaurin, delta 2	hypothetical prote	F14010.2 protein -	vesicular transpor	probable Zn-depend
F81847	S42158	B81082	A81862	686880	A46013	A12223	A71287	S54299	S48821	E96794	C59431	H75165	F86337	B53435	B97180
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535	260	629	629	662	668	670	678	619	944	971	1210	117	739	2550	199
31.4	31.4	31.4	31.4	31.4	31.4	31.4	31.4	31.4	31.4	31.4	31.4	31.1	31.1	31.1	30.7
	44	44	44	44	44	44	44	44	44	44	44	43.5	43.5	43.5	43
44															

ALIGNMENTS

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SULT	멆

RESULT 1
C9HU
Complement C9 precursor [validated] - human
C;Optoment C9 precursor [validated] - human
C;Optoment C9 precursor [man]
C;Date: 27-Nov-1985 #sequence revision 17-Nov-2000 #text_change 09-Jul-2004
C;Date: 27-Nov-1985 #sequence revision 17-Nov-2000 #text_change 09-Jul-2004
C;Accession: A59363; I52400; A91029; A94019; S68647; A59364; A03208
R;Marazitti, D.; Eggertsen, G.; Pey, G.H.; Stanley, K.K.
unpublished results, 1988, cited by GenBank
A;Description: Relationships between the gene and protein structure in human complement.
A;Reference number: A59363

A/Accession: A59363
A/Status: translated from GB/EMBL/DDBJ
A/Status: translated from GB/EMBL/DDBJ
A/Residues: 1-559 cMAR1>
A/Residues: 1-559 cMAR1>
A/Cross-references: UNIPROT:P02748; GB:X02176; NID:g29580; PIDN:CAA26117.1; PID:g29581
R/Marazziti, D.; Beggerteen, G.; Fey, G.H.; Stanley, K.K.
Blochemistry 27, 6529-6534, 1988
A/Title: Relationships between the gene and protein structure in human complement compon A/Reference number: 152400; MUID:89118250; PMID:3219351

A; Accession: I52400

A;Accession: A91029

A; Molecule type: mRNA A; Residues: 'S',1-313,315-559 <STA> A; Creatdues: 'S',1-313,315-559 <STA> A; Creatdues: 'S',1-313,315-559 <STA> A; Creatdues: 'S',1-313,315, ND: 29580 B; DiScripio, R.G.; Gehring, M.R.; Podack, B.R.; Kan, C.C.; Hugli, T.E.; Fey, G.H. Proc. Natl. Acad. Sci. U.S.A. 81, 7298-7302, 1984 Proc. Natl. Acad. Sci. U.S.A. 81, 7298-7302, 1984 A; Title: Nuclectide sequence of cDNA and derived amino acid sequence of human complement A; Reference number: A94019; MUID:85063778; PMID:6095282

A; Molecule type: mRNA A; Residues: 2-12, 'X', 14-16,'X', 18-42,'R', 44-313,315-416,'P', 418-559 < DIS> A; Cross-references: GB: K02766; NID: 9179725; PIDN: AAA51889.1; PID: 9179726 B; Lengweiler, S.; Schaller, J; Rickli, B.E. FBBS Lett. 380, 8-12, 1996 A; Title: identification of disulfide bonds in the ninth component (C9) of human compleme-A; Reference number: \$68647; MUID: 96181657; PMID: 8603752

A;Molecule type: protein
M;Residues: 34-47;52-59;69-87, X', 89-93, 'T', 94-98;106-113;118-131;136-145;180-181, 'X', 18
R;Mitze. Schlomp, K.; Hobart, M.J.; Fernle, B.A.; Orren, A.; Wurzner, R.; Rittner, C.; Ka
Immunogenetics 48, 144-147, 1998

A;Title: Heterogeneity in the genetic basis of human complement C9 deficiency. A;Reference number: A59364; MUID:98298010; PMID:9634479
A;Note: submitted to GenBank, September 1996

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Cyaccesion: PN0494
RyOzawa, Y.; Uchida, K.; Uchida, M.; Ami, Y.; Kushida, S.; Okada, N.; Miwa, M.
RyOzawa, Y.; Uchida, K.; Uchida, M.; Ami, Y.; Kushida, S.; Okada, N.; Miwa, M.
Biophys. Res. Commun. 193, 119-125, 198
Biochem. Biophys. Res. Commun. 193, 119-125, 198
A;Title: Isolation of cDNAs encoding the catalytic domain of poly(ADP-ribose) polymerase 1, A;Reference number: PN0494; MUID:93277538; PMID:8503897
A;Rocession: PN0494
A;References: NUIDROT:008824
A;Residues: 1-135 < OZA>
A;Residues: 1-135 < OZA>
A;Residues: UNIRROT:008824
C;Comment: This zinc-finger protein plays a role in DNA repair, cell growth, and differency C;Comment: This zinc-finger protein plays a role in Experiment of Signerfamily: NADP-ribosyltransferase
C;Keywords: DNA binding; glycosyltransferase; hexosyltransferase; NAD; nucleus; pentosylti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complement C9 precursor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 16-Jul-1999
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 16-Jul-1999
C;Accassion: A29677
R;Stanley, K.K.; Herz, J.
EMBO J. 6, 1951-1957, 1987
A;Title: Topological mapping of complement component C9 by recombinant DNA techniques sug A;Reference number: A29677; MUID:88004404; PMID:2443347
A;Reference number: A29677
A;Roccasion: A29677
A;Roccasion: A29677
A;Roccasion: A29677
C;Superfamily: complement C9; EGF homology; LDL receptor ligand-binding repeat homology; C;Scyvords: complement atternate pathway; complement pathway; cytolysis; glycoprotein; irl C;Superfamin: LDL receptor ligand-binding repeat homology <LDL1>
F;79-112/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;489-518/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E; Accession: AG1117
R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Dominguez-Bernal, G.; Duchaud, B.; Durand, L.; Dussurget, O.; Entian, K.D.; Faihi, H., D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Matlok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Ritle: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID: 21537279; PMID: 11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transketolase homolog 1mo0342 [imported] - Listeria monocytogenes (strain EGD-e)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
                                                                                             NAD ADP-ribosyltransferase (EC 2.4.2.30) - cherry salmon (fragment)
NiAlternate names: poly ADP-ribose polymerase
C.Species: Oncorhynchus masou (cherry salmon)
C,pete: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Match 35.0%; Score 49; DB 2
Local Similarity 50.0%; Pred. No. 2.7;
les 10; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             354 CLGFNMDLRIPLODDLKDASVTASVNADGC 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 LDVSLAFSEISVGAEFNKDD 25
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S:
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
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probable ubiquitin ligase - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Date: 03-Dec-1999
C;Date: 03-Dec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A peacription: in association with complement C5b-8 complex polymerizes to form a transmaperation complement pathway

A; Pathway: complement pathway

B; Pathway: complement C9; BGF homology; LDL receptor ligand-binding repeat homology; C; Superfamaliy: complement C9; BF homology; LDL receptor ligand-binding repeat homology; C; Reywords: complement pathway; cytolysis; glycoprotein; inflammation; membrane attack C; F; 1-21/Domain: signal sequence #status predicted <SIG>
F; 22-265, 266-559/Product: complement C9 #status predicted <C9A>
F; 22-265, Domain: complement C9 #status predicted <C9A>
F; 21-265, Domain: complement C9 #status predicted <C9B>
F; 21-265, Domain: complement C9b #status predicted <C9B>
F; 266-559/Domain: complement C9b #status predicted <C9B>
F; 21-265/Domain: complement C9b #status predicted
F; 266-56/Cleavage site: 2'-mannosyl-tryptophan (Trp) #status predicted
F; 265-266/Cleavage site: His-Gly (thrombin) #status predicted
F; 265-266/Cleavage site: His-Gly (thrombin) #status predicted
A;Accession: A59364
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 27-559 «WIT»
A;Broeximental source: macronuclear; tissue type blood; cell type lymphocyte
B;Hofsteenge, J; Blommers, M; Hess, D; Furmanek, A; Miroshnichenko, O.
A; Biol. Chem. 274, 32796.32794, 1999
A;Tile: The four terminal components of the complement system are C-mannosylated on mul
A;Reference number: A59362; MuID:20020247; PMID:10551839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: identification and location of C-mannosylation sites by mass-spectroscopy and (1
C;Genetics:
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46.2%; Pred. No. 27;
tive 4; Mismatches 10; Indels
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A,Cross-references: GDB:119738; OMIM:120940
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Matches 12; Conservative
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C;Accession: 130493
R;Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohr. Virology 253, 17-34, 1999
A;Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria d A;Reference number: Z20836; MUID:99124785; PMID:9887315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-203 <KUZ>
A,Cross-references: UNIPROT:Q9YMI5; EMBL:AF081810; NID:g3822234; PIDN:AAC70329.1; PID:g3
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R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein ORF143 - Lymantria dispar nuclear polyhedrosis virus C;Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV C;Date: 29-0ct-1999 #sequence_revision 29-0ct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein At2g40200 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Decies: Peb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004 C;Accession: E84826
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C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
                                                                                                                  Gaps
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13;
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7
                                      Score 48; DB;
Pred. No. 22;
5; Mismatches
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1; Mismatches
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123 VGLAIAERTLGAQFNRPD 140
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                                      34.3%;
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Best Local Similarity 38.5'
Matches 10; Conservative
                                                                                                                  Conservative
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Nature 392, 353-358, 1998
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Matches 9; Conserv
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A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Listeria innocua (strain Clip11262)

(Species Listeria innocua
(Species Listeria)
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C,Genetial source: strain Clip11262
C,Genetial Source: A,Gene: lin0360
C,Superfamily: transketolase; thiamin pyrophosphate-binding domain homology
                              A,Residues: 1-665 <GLA>
A,Cross-references: UNIPROT:Q8YA23, GB:NC_003210; PIDN:CAC98421.1; PID:g16409720; GSPDB:
A,Experimental source: strain EGD-e
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C;Genetics:
                                                                                                                                     C,Genetics:
A,Gene: 1mo0342
C;Superfamily: transketolase; thiamin pyrophosphate-binding domain homology
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C;Superfamily: transketolase; thiamin pyrophosphate-binding domain homology
C;Keywords: transferase
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                                                                                                                                                                                                                                                                                           Length 665
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                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                           Query Match

34.3%; Score 48; DB
Best Local Similarity 34.8%; Pred. No. 22;
Matches 8; Conservative 8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
hes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-665 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Rosidues: 1-1372 < MUR>
A;Cross-references: UNIPROT:P91526; EMBL:U80815; PIDN:AAB37995.1; GSPDB:GN00022; CESP:W07.
A;Experimental source: strain Bristol N2; clone W02C12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 1
A;Introns: 14/2; 227/2; 337/3; 544/2; 626/3; 661/1; 776/1; 964/3; 1153/2; 1720/2; 1875/3.,
C;Superfamily: DNA-directed DNA polymerase II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Neisseria meningitidis
C;Species: OS-MAY-2000 #sequence_revision OS-MAY-2000 #text_change O9-Jul-2004
C;Accession: C81822
C;Accession: C81822
R;Parkhill, J; Achtuan, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
sturre 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-2144 <WIL>
A;Cross-references: UNIPROT:062218; EMBL:281526; PIDN:CAB04263.1; GSPDB:GN00019; CESP:F3: A;Experimental source: clone F33H2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  topoisomerase IV subunit B (EC 5.99.1.-) NMA1941 [imported] - Neisseria meningitidis (st:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21712
                                                                                                                        C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 4
A;Introns: 29/1; 66/1; 774/2; 823/2; 1046/1; 1108/2; 1298/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       608 YHLDVGAMYPNIILTNRLQPCAMVTEEICMGCSYNKPD 645
                                                                                                                                                                                                     C; Accession: T25933
R; Murray, J.; Wohldmann, P.
submitted to the EMBL Data Library, December 1996
submitted to the EMBL Data Library, December 1996
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Pred. No. 1.6e+02;
4; Mismatches 7;
                                                                                               hypothetical protein W02C12.1 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F33H2.5 - Caenorhabditis elegans
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A, Status: preliminary; translated from GB/BMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 46; DB 2;
Pred. No. 98;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R, Cottage, A. submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 YHCDCTLGFD--GVHCEMNIDEC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 YHLDVSLAFSEISVGAEFNKDDC 26
                                                                                                                                                                                                                                                                                                     A;Description: The sequence of C. A;Reference number: Z20112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.9%;
al Similarity 28.9%;
11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 32.9%;
Best Local Similarity 43.5%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
A;Gene: CESP:W02C12.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene: CESP: F33H2.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: C81822
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C81822
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A; Experimental source: liver
C; Comment: The amino-terminal 600 residues exhibits homology with those of inter-alpha the c; Comment: The amino-terminal 600 residues exhibits homology with those of inter-alpha the c; Function:
A; Description: highly sensitive to plasma kallikrein
C; Superfamily: inter-alpha-trypsin inhibitor complex component II
C; Keywords: chondrolin sulfate proteoglycan; glycoprotein; serine proteinase inhibitor
F; 1-28/Domain: signal sequence #status predicted <SIG>F; 29-68/Product: inter-alpha trypsin inhibitor heavy chain-related protein #status predicted
F; 81, 207, 577/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 66/Bainding site: carbohydrate (Ser) (covalent) #status predicted
F; 656, 702/Binding site: carbohydrate (Ser) (covalent) #status predicted
F; 701/Binding site: carbohydrate (Thr) (covalent) #status predicted
                                                                                        A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-292 cAQP? A;Residues: 1-292 cAQP? A;Cross-references: UNIPROT: 067397; GB:AE000738; NID:g2983801; PIDN:AAC07368.1; PID:g298 A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 29-44;48-55;61-75;99-111;140-151;163-169;211-224;246-267;274-281;296-329;392
A; Residues: 29-44;48-55;61-75;99-111;140-151;163-169;211-224;246-267;274-281;296-329;392
B; Experimental Bource: liver
FEBS Lett. 357, 207-211, 1995
A; Title: CDNA and deduced amino acid sequence of human PK-120, a plasma kallikrein-sensi
A; Reference number: $68457; MUID:95104473; PMID:7805892
                                                                                                                                                                                                                                                                         C,Genetics:
A,Gene: aq 1392
C,Superfamily: Methanobacterium thermoautotrophicum conserved hypothetical protein MTH13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;cross-references: UNIPROT:Q14624; DDBJ:D38595; NID:g664887; PIDN:BAA07602.1; PID:g1483
A;Accession: PC2355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NyAlternate names: IHRP; plasma glycoprotein
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Apr. 1995 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Datession: JX0368; PC2355; Z68457; S78548
R;Saguchi, K.; Tobe; T.; Hashimoto, K.; Sano, Y.; Nakano, Y.; Miura, N.H.; Tomita, M. J. Blochen. 117, 14-118, 1995
A;Title: Cloning and characterization of cDNA for inter-alpha-trypsin inhibitor family A;Reference number: JX0368; MUID:95293915; PMID:7775381
A,Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A,Reference number: A70300; MUID:98196666; PMID:9537320 A,Accession: C70421
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A;Residues: 1-84,'I',86-113,'S',115-930 <NIS>
A;Cross-references: EMBL:D38535; NID:g624879; PIDN:BAA07536.1; PID:g1402590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inter-alpha-trypsin inhibitor heavy chain-related protein precursor - human
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64.3%; Pred. No. 65;
tive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Length 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 32.9%; Score 46; DB 2;
Best Local Similarity 58.8%; Pred. No. 19;
Matches 10; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 LKYELDFRLAFSAITLG 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 LGYHLDVSLAFSEISVG 18
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-930 <SAG1>
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les 9; Conserv
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-661 < PAR>
A;Cross-references: UNIPROT: 09JT79; GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB8516
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: parE; NMA1941
C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain B
C;Keywords: isomerase
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                                                                                                                                                                                                                                                                                                Query Match 32.5%; Score 45.5; DB 2; Length 661; Best Local Similarity 34.5%; Pred. No. 54; Matches 10; Conservative 5; Mismatches 9; Indels
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Cybecies: Neiseria meningitidis
C;Species: Neiseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: D81055
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.R. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; I., H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.
A;Authors: D81055
A;Accession: D81055
A;Accession: D81055
A;Accession: D81055
A;Accession: D81055
A;Accession: D81057
A;Accession: D81055
A;Grandi C;TET>
A;Cross-references: UNIPROT:Q9JV97; GB:AE002518; GB:AE002098; NID:g7226928; PIDN:AAF4203
A;Experimental source: serogroup B, strain MCS8
C;Genetics:
A;Gene: NMB1682
C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain B

5 Query Match 32.5%; Score 45.5; DB 2; Length 661; Best Local Similarity 34.5%; Pred. No. 54; Matches 10; Conservative 5; Mismatches 9; Indels 5

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Gaps

2 LGYHLD-----VSLAFSEISVGAEFNKDD 25 요

Search completed: June 8, 2005, 10:44:59 Job time: 31.6279 secs

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OM protein - protein search, using sw model

June 8, 2005, 10:24:21; Search time 136.651 Seconds (without alignments) 97.431 Million cell updates/sec Run on:

US-09-020-393B-14_COPY_26_51 140 1 CLGYHLDVSLAFSEISVGAEFNKDDC 26 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Database :

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		d			SUMMAKIES	
Result		Query				
No.	Score	Match	Match Length	8	σī	Description
-		100.0	559	-	CO9 HUMAN	B homo
7	59.5	42.5	547	Н	CO9_HORSE	P48770 equus cabal
m	57	40.7	554	-	CO9_RAT	
4	54	38.6	1050	~	Q8D <u>0</u> 83	Q8d083 yersinia pe
S	54	œ.	1075	~	Q66C38	Q66c38 yersinia ps
9	23	37.9	546	~	Q6YZN1	
7	53	37.9	668	~	Q7UZP8	
Φ	53	37.9	1392	0	Q69Z29	
σ	52	37.1	297	~	Q7ZWY2	
10	52	37.1	557	-	CO9_RABIT	P48747 oryctolagus
11	52		999	~	ОВЕОМЗ	Q8eqm3 oceanobacil
12	52	37.1	3227	-	PTR1 SCHPO	O13834 schizosacch
13	51	36.4	146	~	Q6S4H9	Q6s4h9 human papil
14	51	36.4	1491	~	Q8C115	_
15	50.5	36.1	511	~	Q7VTQ3	
16	50.5	36.1	512	7	Q7WNV3	
17	20	35.7	303	~	Q9EZ31	
18	50	35.7	326	~	051944	
19	50	35.7	326	7	051948	
20	50		326	7	Q9Z4K1	
21	20	35.7	327	~	Q9Z4L5	
22	20		930	7	Q8N3Q3	Q8n3q3 homo sapien
23	20	35.7	1449	7	Q8IVE3	
24	49	S		Н	PPOL ONCMA	_
25	49	S		н	CO9 MOUSE	P06683 mus musculu
26	49	ď.	573	~	Q7Q2F2	Q7q2f2 anopheles g
27	49	35.0	893	~	QBPTLO	_
28	48	34.3	999	7	Q8YA23	Q8ya23 listeria mo
29	48	34.3	, 665	7	Q92EU8	~
30	48	34.3	665	7	Q723W3	
31	48	34.3	999	0	Q8Z4S9	Q8z4s9 salmonella

	Q7sd09 neurospora Q63qs1 burkholderi Q62h05 burkholderi	0923v8 rattus norv Q6fws9 candida gla	Q8mnw6 caenorhabdi Q9i712 drosophila	-	Q6bd08 drosophila Q6bd09 drosophila	Q6bd16 drosophila
Q8ZN82 Q8D1X4	Q7SD09 Q63QS1 Q62H05	SE15 RAT Q6FWS9	Q8MNW6 Q917L2	Q6BD05 Q6BD06	Q6BD08 Q6BD09	Q6BD16
~ ~	000	40	~ ~	0 0	0 0	0
999	675 675 690	162 3108	176 241	324 324	324 324	324
34.3	34.3 34.3 4.3	33.9	33.6 33.6	33.6 33.6	33.6 33.6	33.6
4 4 8 8	4 4 4 8 8 8	47.5	47	47	4 47	47
32	334 36	37 38	939 04	41	4 4 4	45

ALIGNMENTS

RESULT CO9_HU	RESULT 1 CO9 HUMAN ID CO9 HUMAN	STANDARD;	∿RD;	PRT;	559 AA.	
N T T	P02748; 21-JUL-1986 01-FEB-1996	(Rel. 01,	Creat	ed) seguence update)	indate)	
日日	05-JUL-2004 Complement c			notation rsor.	Last annotation update)	
S G	Name=C9;	(C.				
88	Fukaryota; Metazoa;	etazoa; (Chordata;	Craniata;	a, Verte	Vertebrata; Euteleostomi;
88	Mammalia; Eutheria; NCBI TaxID=9606;		Primates;	Catarr	nini; Hom	Catarrhini; Hominidae; Homo.
RN C	[1]					
ž ž	SEQUENCE FROM N.A. MEDLINE=85257464; PubMed=4018030;	M N.A. 7464; Pul	oMed=4018	030;		•
RA E	Stanley K.K., Kocher HP., Luzio J.P., Jackson P	, Kocher	HP., L	uzio J.	P., Jacks	Luzio J.P., Jackson P., Tschopp J.;
Z.Z	EMBO J. 4:37	4:375-382 (1985).	35).	TI MILITARIA	Tomo Tomo	(Danielle C
Z G	[2] SECTENCE FROM N.A.	4 2				
RC	TISSUE=Liver;					
X :	MEDLINE=2238	8257; Pul	OMed=1247	7932; D	N=10.107	MEDLINE-22388257; PubMed=12477932; DOI-10.1073/pnas.242603899;
Z i	Strausberg R	.L., Fell	R.L., Feingold E.A.,	., Grou	3е г.н.	
8 8	Klausner R.D Altschul S.F	., Collii Zeebe	18 F.S., rq B., Bu	wagner etow K.1	c., Shenm	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
æ	Hopkins R.F.	, Jordan	H., Moor	e T., X	3X S.I.,	Wang J., Hsieh F.,
RA:	Diatchenko L	., Marus	ina K., F	armer A	.A., Rubi	
R A	Stapleton M. Brownstein M	, Soares	M.B.,	naldo M Toshivul	ci S. Casa	vant T.L., Scheetz T.E., rninci P., Prange C.,
R.	Raha S.S., L	oquellano	N.A., P	eters G	J., Abra	mson R.D., Mullahy S.J.,
æ	Bosak S.A.,	McEwan P	J., McKe	rnan K.	J., Malek	atne P.
8 8	Richards S.,	Worley	K.C., Hal	e S., G	arcia A.M	I., Gay L.J., Hulyk S.W.,
5 2	Fahev J., He	lton E.,	Ketteman	M., Max	an A., R	Villaton D.A., Muzny D.M., Sodergren E.O., Lu A., Gibbs K.A., Fahev J., Helton E., Ketteman M., Madan A., Rodriques S., Sanchez A.,
æ	Whiting M.,	Madan A.	Young A	.c., Sh	evchenko	G.G.,
8 8	Blakesley R.	W., Touch	man J.W.	Green	E.D., Di	CKSON'M.C.,
5 5	Butterfield	Y.S.N., 1	Krzywinsk	i M.I.,	Skalska	Skalska U., Smailus D.E.,
R.	Schnerch A.,	Schein	J.E., Jon	es S.J.1	4., Marra	M.A.;
RT T	"Generation	on and initial ana	ial analy	sis of 1	nore than	analysis of more than 15,000 full-length human
RL		Acad. Sc.	i. U.S.A.	99:168	99-16903 (2002).
RN	[3]					
КР	SEQUENCE OF	2-559 FROM N.A.	OM N.A.			
2 Z	MEDLINE=85063778; PubMed=6095282;	3778; Pul	oMed=6095	282; Dodack	T Kan	MEDLINE=85063778; PubMed=6095282; Discipio D Cobring M D Dodack 報 B Kan C C Hugli T R
5 S	Fey G.H.;	1 11100			1.4.9	:
RT	"Nucleotide sequence of cDNA	seguence	of cDNA	and	derived amin	amino acid sequence of human
RI.	<pre>complement component C9."; Proc. Natl. Acad. Sci. U.S.A.</pre>	omponent Acad. Sc:	C9.";		81:7298-7302 (1984)	84).
R.N	[4]					
RP ox	SEQUENCE OF 62-159 FROM N.A. MEDLINE-89118250: DibMed-3219351:	62-159 FROM N.A.	ROM N.A.	251.		
Ş	MEDLINE=0711	m= (007p	OMCC=5217	, 100		

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GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0019836; P:hemolysis; TAS.
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CO9_HORSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=8603752; DOI=10.1016/0014-5793(95)01541-8;
Lengweiler S., Schaller J., Rickli B.E.;
Lengweiler S., Schaller J., Rickli B.E.;
T "Identification of disulfide bonds in the ninth component (C9) of
T human complement.";
FEBS Lett. 380:8-12(1996).

-!- FUNCTION: C9 is the final component of the complement system to be added in the assembly of the membrane attack complex. It is able to enter lipid bilayers, forming transmembrane channels.

-!- FTM: Thrombin cleaves factor C9 to produce C9a and C9b.
-!- PTM: Thrombin cleaves factor C9 to produce C9a and C9b.
-!- DISABSE: Defects in C9 are a cause of component C9 deficiency c C9D) [MIM:120940]. Patients with C9D suffer from recurrent bacterial infections, predominantly from Neisseria meningitidis.
-!- SIMILARITY: Contains 1 EGF-like domain.
-!- SIMILARITY: Contains 1 LDB-receptor class A domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Localization and molecular modelling of the membrane-inserted domain of the ninth component of human complement and perforin."; Mol. Immunol, 27:589-602(1990),
                                                                                                                                                                  SEQUENCE OF 27-559 FROM N.A., AND VARIANT C9D GLY-119.
MEDLINE-98298010; PubMed=9634479; DOI=10.1007/8002510050415;
Witzel-Schloemp K., Hobart M.J., Fernie B.A., Orren A., Wuerzner R.,
Rittner C., Kaufmann T., Schneider P.M.;
"Heterogeneity in the genetic basis of human complement C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20020247; PubMed=10551839; DOI=10.1074/jbc.274.46.32786; Hofsteenge J., Blommers M., Hess D., Furmanek A., Miroshnichenko O.; "The four terminal components of the complement system are C-mannosylated on multiple tryptophan residues."; Biol. Chem. 274:32786-32794 [1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90370039; PubMed=2395434; DOI=10.1016/0161-5890(90)90001-G;
Peitsch M.C., Amiguet P., Guy R., Brunner J., Maizel J.V. Jr.,
Marazziti D., Eggertsen G., Fey G.H., Stanley K.K.; "Relationships between the gene and protein structure in human complement component C9."; Biochemistry 27:6529-6534 (1988).
                                                                                                                                                                                                                                                                                                                                                                                                                     [6]
3D-STRUCTURE MODELING OF MEMBRANE-SPANNING DOMAIN (MSB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X02176; CAA26117.1; -. EMBL; BC020721; AAH20721.1; -. EMBL; K02766; AAA31889.1; -. EMBL; Y028545; CAA51889.1; -. EMBL; Y08545; CAA69849.1; -. EMBL; Y08546; CAA69849.1; JOINED. EMBL; Y08549; CAA69849.1; JOINED. EMBL; Y08549; CAA69849.1; JOINED. EMBL; Y08549; CAA69849.1; JOINED. EMBL; Y08550; CAA69849.1; JOINED. EMBL; Y08550; CAA69849.1; JOINED.
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EMBL; Y08552; CAA69849.1; JOINED.
EMBL; Y08553; CAA69849.1; JOINED.
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HSSP; Q07954; ICRB.
Genew; HGNC:1358; C9.
H-INVB; HXC004829; -.
MIM; 120940; -.
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                                                                                                                                                                                                                                                                                                                                                  deficiency."
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C-linked (Man); partial.
N-linked (GlCNAc. . ) (Probable).
N-linked (GlCNAc. . ) (Probable).
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                                                                                                                                                                                                                                                                                    Complement alternate pathway, Complement pathway, Cytolysis, Disease mutation; EGF-like domain; Glycoprotein; Membrane attack complex; Plasma; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 140; DB 1; Length 559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C -> G (in C9D).
/FTId=VAR 012648.
C -> R (in Ref. 3).
Missing (in Ref. 3).
T -> P (in Ref. 3).
W; 7403F6AD77B3ECEI CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                 Complement component C9a.
Complement component C9b.
TSP type-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cleavage (by thrombin)
                                                                                                                                                                                                                                                                                                                                                                                                                                        LDL-receptor class A. Potential.
                                                                                                                                                                                                                                                                                                                                                                  Complement component
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01-FEB-1996 (Rel. 33, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Complement component C9 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C-linked (Man).
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0; Mismatches
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InterPro; IPR006209; EGF like.
InterPro; IPR002172; LDL receptor_A.
InterPro; IPR001172; LDL receptor_A.
InterPro; IPR001862; MAC_Perforin.
InterPro; IPR001864; TSP1.
Pfam; PF001057; Ldl recept_a; 1.
Pfam; PF010823; MAC_PF; 1.
Pfam; PF001090; TSP 1; 1.
PRINTS; PR00764; COMPLEMENTC9.
PRINTS; PR00764; COMPLEMENTC9.
PROSITE; PS001026; EGF 1; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS010209; LDLRA 1; 1.
PROSITE; PS0010209; LDLRA 2; 1.
PROSITE; PS001029; TSP1; 1.
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Les 26; Conservative
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417 4
559 AA;
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1 CLGYHLDVSLAFSEISVGAEFNKDDC 26
                                                                                                                                                                                                                                                                                                                                         Name=C9;
     ò
                                                                  MEDLINE-95325619; PubMed=7541424;

MEDLINE-95325619; PubMed=7541424;

A Tomlinson S., Wang Y., Ueda E., Esser A.F.;

Sequence in horse C9 responsible for restriction of hemolysis.";

J. Immunol. 155:43-444(1955).

C -!- FUNCTION: C9 is the final component of the complement system to be added in the assembly of the membrane attack complex. It is able.

C -!- FUNCTION: C9 is the final component of the complement complex.

C -!- FUNCTION: Secreted.

C -!- FTM: Thrombin cleaves factor C9 to produce C9a and C9b.

C -!- FTM: Thrombin cleaves factor C9 to produce C9c and C9b.

C -!- FTM: Thrombin cleaves factor C9 to produce C9c and C9b.

C -!- SIMILARITY: Contains 1 EGF-like domain.

C -!- SIMILARITY: Contains 1 LSP type-1 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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By sim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complement alternate pathway, Complement pathway, Cytolysis,
EGF-like domain, Glycoprotein, Membrane attack complex; Plasma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.5%; Score 59.5; DB 1; Length 547; 46.2%; Pred. No. 1.6; 1.ive 7; Mismatches 6; Indels 1
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75E5FE961DE873B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complement component C9.
TSP type-1.
  Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDL-receptor class A.
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Potential.
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InterPro; IPR00172; LDL_receptor A.
InterPro; IPR001862; MAC_perforin.
InterPro; IPR001862; MAC_perforin.
Pfam; PF00057; Ldl recept_a; 1.
Pfam; PF01823; MACPF; 1.
Pfam; PF00090; TSP_l; 1.
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PROSITE; PS01186; EGF_2; FALSE_NEG.
PROSITE; PS01209; LDLRA_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PSS0068; LDLKA 2; 1.
PROSITE; PSS00279; MAC PERFORIN; 1.
PROSITE; PSS0092; TSPI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00764; COMPLEMENTC9.
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547 AA;
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TRANSMEM
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Gaps

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Conservative

Local Similarity tes 12; Conserv

Best Loc Matches

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                                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                               STRAIN=Sprague-Dawley;
MEDLINE=9735567; PubMed=9212048;
MEDLINE=9735567; Wal z Lbw., Wilson J.L., Jung E., Calisi C.R.,
Goldsmith L.J., Wilson R.A., Morgan B.P., Feldhoff R.C.;
"The administration of complement component C9 enhances the survival
of neonatal rats with Escherichia coli sepsis.";
Pediatr. Res. 42:128-136(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complement alternate pathway, Complement pathway, Cytolysis; EGF-like domain; Glycoprotein; Membrane attack complex; Plasma; Signal; Transmembrane.

Signal; Transmembrane.

Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Sprague-Dawley;
Hinchliffe S.J., Van den Berg C.W., Rushmere N.K., Morgan B.P.
"Cloning of rat C9: consequences for homologous restriction of
                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                          554 AA
380 CLGFNLDLSLK-DKYEVTAKIDKNDC 404
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InterPro; IPR002172; LDL_receptor_A.
InterPro; IPR001862; MAC_perforin.
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PROO764; COMPLEMENTC9.
PROSITE; PSO0022; EGF 1; 1.
PROSITE; PSO1186; EGF 2; FALSE_NEG.
PROSITE; PSO1209; LDLRA 1; 1.
PROSITE; PSS0068; LDLRA 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U49071; AAB38023.1; -.
EMBL; U52948; AAA96528.1; ALT_INIT.
HSSP; Q07954; 1J8E.
                                                                                                                                                                     Complement component C9 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50068; LDLRA-2; 1.
PROSITE; PS00279; MAC PERFORIN; 1.
PROSITE; PS50092; TSPI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00057; Ldl recept_a; 1.
Pfam; PF01823; MACPF; 1.
Pfam; PF00090; TSP_1; 1.
                                                                                         STANDARD;
                                                                                                                                                                                                    Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                             NCBI_TaxID=10116;
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                                                                                                         Q62<u>9</u>30; Q62957;
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PubMed=1536885;

XPAIN=IP 3205.

PubMed=1536885;

XA Chain P.S.G. Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,

Chain P.S.G. Carniel E., Larimer F.W., Land M.L., Motin L.V.,

Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin L.V.,

A Simonet W., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M.,

Derbise A., Hauser L.J., Garcia E.,

Insights into the genome evolution of Yersinia pestis through whole genome comparison with Yersinia pseudotuberculosis.";

Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).

R InterPro; IPR003544; Big_1.

InterPro; IPR003555; Intimin.

R Fam: PPO.3189; Big_1;

R FAM: SMO6349; INVASin_intimin.

R FAMT; SMO634; Big_1;

R SMART; SMO634; BID_1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Hypothetical protein P0426E02.8 (Hypothetical protein
B1104607.30).
Name=P0426E02.8; Synonyms=B1104G07.30;
Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                              Yersinia pseudotuberculosis IP 32953.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae; Yersinia.
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Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 Potential.
114564 MW; AF94B11B71D4AB38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sasaki T., Matsumoto T., Katayose Y.; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sasaki T., Matsumoto T., Katayose Y.; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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                                                                                                                                                                           PRT; 1075 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 LGYNLFVDHDASYSHTRIGVGAEYGRD 207
                               181 LGYNLFIDHDASYSHTRIGVGAEYGRD 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 LGYHL----DVSLAFSEISVGAEFNKD 24
  2 LGYHL----DVSLAFSEISVGAEFNKD 24
                                                                                                                                                                                                                            Created)
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Matches 12; Conservative
                                                                                                                                                                                                                       25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                Putative invasin precursor.
ORFNames=YPTB1572;
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                                                                                                                                                                           PRELIMINARY;
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SEQUENCE 1075 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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QEYZN1
                                                                                                                       RESULT 5
Q66C38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22137863; PubMed=1242430; MEDLINE=22137863; PubMed=1242430; DOI=10.1128/JB.184.16.4601-4611.2002; Dong W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R., Perry R.D.; "Genome sequence of Yersinia pestis KIM.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Potential). (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 57; DB 1; Length 554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR01369; INTIMIN.
SMART; SM00634; BID 1; 3.
SEQUENCE 1050 AA; 111967 MW; 7C215A33E9B013B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9C885F76A1275649 CRC64;
                                                                                                                                                                      By similarity.
No by similarity.
By 
Complement component C9. TSP type-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                         EGF-like.
Cleavage (by thrombin)
                                                   LDL-receptor class A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -> M (in Ref. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              382 CLGFNLDVSLYTPLQTALEGPSLTANVNHSDC 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CLGYHLDVSL-----AFSEISVGAEFNKDDC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1050 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 4;
3; Mismatches
                                                                        Potential.
Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003344; Big_1.
InterPro; IPR003535; Intimin.
InterPro; IPR008964; Invasin_intimin.
Pfan; PF02369; Big_1; 3.
PRINTS; PR01369; INTIMIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Bacteriol. 184:4601-4611(2002).
EMBL; AE013862; AAM86159.1; -.
GO; GO:0007155; P:cell adhesion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=KIMS / Biovar Mediaevalis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62280 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25, Putative adhesin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 43.8
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 44.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OrderedLocusNames=y2605;
  554 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yersinia pestis
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                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
DISULFID
CARBOHYD
                                                                      TRANSMEM
TRANSMEM
DOMAIN
                                                                                                                                                   SITE
DISULFID
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CARBOHYD
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                                                                                                                                                                                                                                                   DISULFID
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CHAIN
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Matches
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090083
1008083
1008083
01-0080
01-0080
01-0080
02 Yers
03 Yers
03 Yers
04 Yers
05 Bact
06 Bact
07 Yers
08 Yer
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Gaps

4

Indels

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25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                       NCBI_TaxID=10090;
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                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome divergence in two Prochlorococcus ecotypes reflects oceanic niche differentiation.";
Nature 424:1042-1047(2003).
BENBL; BX572094; CAE20069.1; --.
HSSP; P23254; 1AY0.
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
Johnson Z.I., Land M.L., Lindell D., Poet A.F., Regala W., Shah M.,
Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
Webb B.A., Zinser B.R., Chisholm S.W.;
                                                                                                                                                                                                                                                                                             Name=tktA; Synonyms=cbbT; OrderedLocusNames=PMM1610;
Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).
Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
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0
                                                                                   37.9%; Score 53; DB 2; Length 546; 41.7%; Pred. No. 17; ive 7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.9%; Score 53; DB 2; Length 668; 52.6%; Pred. No. 20;
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                                                            546 AA; 61147 MW; 9688ED4409BB7A4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70C7177DDF431FFB CRC64;
                                                                                                                                                                                                                                             01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Transketolase (EC 2.2.1.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO, GO:0016740; F:transferase activity; IEA.
GO; GO:0004802; F:transketolase activity; IEA.
InterPro; IPR005478; BacTransketolase.
InterPro; IPR005476; Transketolase.CR.
InterPro; IPR005476; Transketolase.N.
InterPro; IPR005474; Transketolase.N.
InterPro; IPR005474; Transketolase.N.
InterPro; IPR009014; Transketolase.N.
InterPro; IPR009014; Transketolase.N.
IPFam; PF02789; Transketolase.N; I.
Pfam; PF02789; Transketolase.N; I.
TIGRRAMS; TIGRR00232; tktlase bact; I.
PROSITE; PS00801; TRANSKETOLĀSE 1; I.
PROSITE; PS00801; TRANSKETOLĀSE 2; I.
                                                                                                                                                                                                                       668 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1392 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                 ||:|:|:|:||
455 LGHHGEVAKHFADLCKGAVFDADD 478
                                                                                                                                   2 LGYHLDVSLAFSEISVGAEFNKDD 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                      PRT;
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130 VGLAIAEAHLAAKFNKKDC 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome, Transferase.
SEQUENCE 668 AA; 72987 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 VSLAFSEISVGAEFNKDDC 26
                      InterPro; IPR004158; DUF247.
Pfam; PF03140; DUF247; 1.
Hypothetical protein.
SEQUENCE 546 AA; 61147 MM
 EMBL; AP005520; BAD03752.1;
            EMBL; AP005096; BAD03478.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 28, (TrEMBLrel. 28,
                                                                                                Best Local Similarity 41.7
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Conservative
                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=59919;
                                                                                                                                                                                                                                                                                                                                   Prochlorococcus
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Q69Z29;
25-OCT-2004 (
25-OCT-2004 (
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                                                                                    Query Match
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Q69229
ID Q692
AC Q692
DT 25-00
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Nagase T., Ohara O., Koga H.;
Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene:
IV. The Complete Nucleotide Sequences of 500 Mouse KIAA-Homologues
CDNAs Identified by Screening of Terminal Sequences of cDNA Clones
Randomly Sampled from Size-Fractionated Libraries.";
I. SIMILARITY: Contains 2 PH domains.

EMBL: AKI7337; BAD32615.1; -.
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MEDINE-21388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDINE-21388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkinns R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
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Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1392 AA; 156192 MW; B7CC2971EEED711E CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               297 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005856; C:cytoskeleton; IEA.
GO; GO:0003779; F:actin binding; IEA.
GO; GO:0003774; F:art binding; IEA.
GO; GO:0003774; F:motor activity; IEA.
InterPro; IPR00299; Band 4.1.
InterPro; IPR009065; FERM.
InterPro; IPR001849; PH.
InterPro; IPR011036; PH.
Pfam; PF00169; PH; 1.
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Xenopus laevis (African clawed frog)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50057; FERM 3; 1.
PROSITE; PS5003; PH DÖMAIN; 2.
NON TER 1 1 1 1 1 SEQÜENCE 1392 AA; 156192 MW;
MKIAA2028 protein (Fragment)
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43.5%;
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SMART; SM00139; MyTH4; 1.
SMART; SM00233; PH; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 43.59
Watches 10; Conservative
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                                                            Mus musculus (Mouse)
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Usage by
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           modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              385 CLGFDLDLSLNIPGKSAGLSLTGQANKNNC 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potential.
Potential.
EGF-like.
                                                       or send an email to license@isb-sib.ch).
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                                                                                                                                       InterPro; IPR006209; EGF_like.
InterPro; IPR002102; LDL_receptor_A.
InterPro; IPR001862; MAC_perforin.
InterPro; IPR000884; TSPI.
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01-MAR-2003 (TrEMBLrel. 23, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                         PS00279; MAC PERFORIN; 1. PS50092; TSP1; 1.
                                                                                                                                                                                                                         Pfam; PF00057; Ldl recept_a; 1. Pfam; PF01823; MACPF; 1. Pfam; PF00090; TSP 1; 1. PRINTS; PR00764; COMPLEMENTC9. PRINTS; PR000261; LDLRECEPTOR. PROSITE; PS01186; EGF 1; 1. PROSITE; PS01186; EGF 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62662 MW;
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PROSITE; PS01209; LDLRA_1; 1.
PROSITE; PS50068; LDLRA_2; 1.
                                                                                               EMBL; U20055; AAC48459.1; -. HSSP; Q07954; 1CR8.
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9595
1137
3359
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1126
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536
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557 AA;
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PROSITE;
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DISULFID
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DOMAIN
DOMAIN
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRAINS NOW Zealand white; TISSUE-Liver;

MEDLINE=95181293; PubMed=7533152; DOI=10.1074/jbc.270.8.3483;

MEDLINE=95181293; PubMed=7533152; DOI=10.1074/jbc.270.8.3483;

T. Chimeras of human complement C9 reveal the site recognized by complement regulatory protein CD59.";

T. Complement regulatory protein CD59.";

J. Biol. Chem. 270.3483-3486(1995).

C. -- FUNCTION: C9 is the final component of the complement system to b added in the assembly of the membrane attack complex. It is able to enter lipid abliayers, forming transmembrane channels.

C. -- SUNCELULAR LOCATION: Secrete C9 to produce C9a and C9b.

-- FTM: Thrombin cleaves factor C9 to produce C9a and C9b.

-- FTM: Thrombin cleaves factor C9 to produce C9 and C9b.

-- FTM: Thrombin cleaves factor C9 to produce C9 and C9b.

-- SIMILARITY: Contains 1 EGF-like domain.

-- SIMILARITY: Contains 1 LDL-receptor class A domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                    Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                              Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                        Match 37.1%; Score 52; DB 2; Length 297; Local Similarity 43.5%; Pred. No. 13; es 10; Conservative 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Embryo;
Klein S., Strausberg R.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO46655, AA446655.1;
InterPro; IPR008978; HSP20 chap.
SEQUENCE 297 AA; 33656 WW; FD17E16D9BFC7C28 CRC64;
                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FFB-1996 (Rel. 33, Created)
01-FFB-1996 (Rel. 33, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complement component C9 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                       Dev. Dyn. 225:384-391(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 [3]
SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     initiative.",
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P48747;
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Best Local 9
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1009 RABIT

AAC P4874 P4874 P4874 P4877 P48
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(See http://www.isb-sib.ch/announce/
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Name=tkt; OrderedLocusNames=OB1672;
Oceanobacillus iheyensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complement alternate pathway; Complement pathway; Cytolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 557;
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Takami H., Takaki Y., Uchiyama I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct protein sequencing, EGF-like domain, Glycoprotein,
Membrane attack complex, Plasma, Signal; Transmembrane.
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TSP type-1.
LDL-receptor class A.
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SEQUENCE
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RRARAR RR
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MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
MEDLINE=21848401; PubMed=11859360; Davis B. V. Dawman D., Bowman S., Davis B. V. Bowman D., Bowman S., Davis B. V. Etwell T. R. Churcher C.M., Collins M., Connor R., Cronin A., Davis B. V., Feltwell T., Fraser A., Dentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., MoDonald S., McLean J., Dames K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., Andrew R., Squares S., Stevens K., Alvis Skelton J., Simmonds M., Squares B., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Weltight J., Vanstreels E., Rieger M., Schaefer M., Maeller-Auer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Benthardt R., Pohl T.M., Beger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Albers M., Rochet M., Galibaridin C., Tallada V.A., Garzon A., Thode G., Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last amoutation update)
E3 ubiquitin protein ligase ptrl (EC 6.3.2.-) (Poly(A)+ RNA transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
'Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
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45.5%; Pred. No. 29;
tive 4; Mismatches 8; Indels
                            its unexpected adaptive capabilities to extreme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 666 AA; 73151 MW; 710EE8B905A6DFF0 CRC64;
                                                              Mucleic Acids Res. 30:3927-3935(2002).

EMBL; AP004598; BAC13628.1; -.
HSSP; P27302; 1QGD.
GG:0004802; F:transketolase activity; IEA.
InterPro; IPR005478; BacTransketolase.
InterPro; IPR005476; Transketolase.
InterPro; IPR005476; Transketolase.
InterPro; IPR005476; Transketolase.
InterPro; IPR005476; Transketolase.
InterPro; IPR00904; Transketolase.
InterPro; IPR00557; Transketolase.
INTERPAMS; TRANSKETOLASE.
INTERPAMS; INTERPOSE.
INTERPAMS; INTERPOSE.
INTERPAMS; IPR00557; TRANSKETOLASE.
INTERPAMS; IPR055057; TRANSKETOLASE.
INTERPROSITE; PS008061; TRANSKETOLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 3227 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GYHLDVSLAFSEISVGAEFNKD 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein 1).
Name=ptr1; ORFNames=SPAC19D5.04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 45.5
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome. SEQUENCE 666 AA;
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013834;
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PTR1_SCHPO
RATTANDOR STATE
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                                                                                                                              When the transport of the proteins are in Early and murany print.

The fission yeast pirit gene involved in nuclear mRNA export encodes a putative ubiquitin ligase.";

Bachem. Biophys. Res. Commun. 317:1138-1143(2004).

The fission yeast pirit gene involved in nuclear mRNA export encodes a putative ubiquitin ligase.";

Bachem. Biophys. Res. Commun. 317:1138-1143(2004).

The fission yeast print ligase.";

Bachem. Biophys. Res. Commun. 317:1138-1143(2004).

The fission yeast print ligase protein involved in mRNA export. Es ubiquitin ligase protein involved in mRNA export from the nucleus by regulating the transport of hnRNP proteins such as rael.

The ATHWAY: Ubiquitin conjugation; third step.

SUBJECTIVILAR LOCATION: Nuclear.

SIMILARITY: Belongs to the TOMI/PTR1 family.

SIMILARITY: Contains 1 HECT-type E3 ubiquitin-protein ligase
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Ubiquitin (By similarity).
L->Q: In ptr1-1; induces defects in mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakcvski G.V., Ussery D., Barrell B.G., Nurse P.; "The genome sequence of Schizosaccharomyces pombe."; Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3227;
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Human papillomavirus.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00119; HECTc; 1.
PROSITE; PS50237; HECT; 1.
Ligase; mRNA transport; Nuclear protein; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 52; DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
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GeneDB SPombe; SPAC19D5.04; -.
InterPro; IPR010309; DUF908.
InterPro; IPR010314; DUF913.
InterPro; IPR005569; HECT_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z99531; CAB16714.1; -. PIR; T37964; T37964.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.28;
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Pfam; PF06025; DUF913; 1.
Pfam; PF00632; HECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 46.2
nes 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ubl conjugation pathway.
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NCBI_TaxID=10566;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain.
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OG DT OGS
OG DT OGS
OG VI
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NCBI_TaxID=520;
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MEDLINE=204993914; Pubmed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Miramateu M., Hayashizaki Y., "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR.2003 (TrEMBLrel. 23, Created)
01-MAR.2003 (TrEMBLrel. 23, Last sequence update)
01-MAR.2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched
library, clone:4831441H15 product:hypothetical Scrine-rich region/Band
4.1 family/PH domain profile/Core domain in kinesin and myosin
motors/Pleckstrin homology (PH) domain containing protein, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CS7BL/60; TISSUB=Head;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Functional annotation of a full-length mouse cDNA collection.";
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SEQUENCE FROM N.A.

Forslund O., Hradil E., Nordin P., Stenquist B., Kirnbauer R., Slupetekky K., Lindelof B., Dillner J.;

Slupetekky K., Lindelof B., Dillner J.;

Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AY468416; AAR30925.1; ...

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:005198; F:structural molecule activity; IEA.

InterPro; IPR002210; PV capsid_L1.

Pfam; PF00500; Lac procein_L1; 1.

PRINTS; PR00865; HPVCAPSIDL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 51; DB 2; Length 146;
Pred. No. 9.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6: Indels
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                        146 AA; 16331 MW; 32190C2E457541EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1491 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 IGEHWDV----AKPCAGAQFNKGDC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LGYHLDVSLAFSEISVGAEFNKDDC 26
                                                                                                                                                                                                                                                                                                                                            ProDom; PD000544; PV_capsid_L1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Plekhh2; Synonyms=AI256725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Head;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 36.4%;
Best Local Similarity 44.0%;
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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EMBL, AK029252; BMC26356.1; -.
STRAIN=C57BL/6J; TISSUE=Head;
MEDLINE=20530913; PubMed=1107686J; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamanoto R., Matumnoto H., Sakaguchi S., Ikegami T., Rashinagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara B., Watahiki M., Foneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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OrderedLocusNames=BP3462;
Bordetella pertussis.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1491;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:2146813; Plekhh2.
GO; GO:0005856; C:cytoskeleton; IEA.
GO; GO:0003779; F:actin binding; IEA.
GO; GO:0003774; F:motor activity; IEA.
GO; GO:0003774; F:motor activity; IEA.
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InterPro; IPR000065; PERM.
InterPro; IPR000857; WyTH4.
InterPro; IPR001849; PH.
InterPro; IPR010136; PH. related.
Pfam; PP00784; MyTH4; 1.
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PROSITE; PS50003; PH_DOMAIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Head;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alcaligenaceae; Bordetella.
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SMART; SM00139; MyTH4; 1.
SMART; SM00233; PH; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
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REC STRAIN-Tohama I / ATCC BAA-589 / NCTC 13251;

REC STRAIN-Tohama I / ATCC BAA-589 / NCTC 13251;

REC MEDLINE-22827954; PubMed=12910271; DOI=10.1038/ng1227;

RA PATKHILI J., Sebahina M., Preston A., Murphy L.D., Thomson N.R.,

RA Harris D.E., Holden M.T.G., Churcher C.M., Baron N., Cherevach I.,

RA Achtman M., Aktin R., Baker S., Basham D., Harris B., Quail M.A.,

RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

Rabbinowitsch E., Norberczak H., O'Neil S., Ormond D., Price C.,

RA Rabbinowitsch E., Rutter S., Sanders M., Squares S., Stevens K.,

Rabbinowitsch E., Multer S., Barrell B.G., Maskell D.J.;

Romparative analysis of the genome sequences of Bordetella pertussis,

RT Comparative analysis and Bordetella bronchiseptica.";

RT Bordetella parapertussis and Bordetella bronchiseptica.";

RT Bordetella M.C.C.

RT Barter S. IPRO1079; M.C.C.

RT Bordetella Prostonome: Hypothetical protein.

RM Pfam; PPO711; MIrC C; 1.

Complete proteome; Hypothetical protein.

SEQUENCE SII AA; 54878 MW; FFISCA11D998C599 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.1%; Score 50.5; DB 2; Length 511; 60.0%; Pred. No. 39; tive 4; Mismatches 3; Indels 1
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Search completed: June 8, 2005, 10:44:06 Job time : 138.651 secs

2 LGYHLDVSLAFSEISVGAEF 21

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Best Local Similarity 60.0 Matches 12; Conservative

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Gaps 1; . * .

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8, 2005, 10:24:06 ; Search time 143.302 Seconds (without alignments) 70.172 Million cell updates/sec
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                            OM protein - protein search, using sw model
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                                                                                                                                           June
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US-09-020-393B-14_COPY_26_51

140 1 CLGYHLDVSLAFSEISVGAEFNKDDC 26 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

2105692

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:*geneseqp2003bs:* A_Geneseq_16Dec04:* geneseqp1980s:* geneseqp1990s:* geneseqp2004s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Resı

scrip	Aay27328 Human C9	Aay27324 Human C9	_	Abm83944 Human dia	Abm83943 Human dia	Aaw18310 Human com	Aay27325 Rabbit C9	Abu43379 Protein e	Aaw18311 Rabbit co	Abu21387 Protein e	Adf55468 Human nov	Abu25340 Protein e	Abo71707 Pseudomon	Abo55228 Human gen	Abp39673 Staphyloc	ະດ	Adn19420 Bacterial	Abul6669 Protein e		Abb48204 Listeria	Abu47082 Protein e	Abu22543 Protein e	Aay72637 Exophiala	Aae26387 Exophiala	
ID	AAY27328	AAY27324	ADR20062	ABM83944	ABM83943	AAW18310	AAY27325	ABU43379	AAW18311	ABU21387	ADF55468	ABU25340	ABO71707	AB055228	ABP39673	ADS05775	ADN19420	ABU16669	ADA35154	ABB48204	ABU47082	ABU22543	AAY72637	AAE26387	
DB	2	~	Φ	œ	ω	7	7	9	~	9	7	9	7	80	Ŋ	œ	œ	9	9	ഗ	9	ø	4	ហ	,
Query Match Length DB	27	82	474	522	522	260	86	278	561	405	1449	276	417	63	304	304	363	662	663	665	999	069	1263	1263	
Query	100.0	100.0	100.0	100.0	100.0	100.0	37.1	37.1	37.1	36.4	35.7	35.0	34.6	34.3	34.3	34.3	34.3	34.3	34.3	34.3	34.3	34.3	34.3	34.3	,
Score	140	140	140	140	140	140	52	52	52	51	20	49	48.5	48	48	48	48	48	48	48	48	48	48	48	•
sult No.	1	7	m	4	Ŋ	9	7	ω	σ	10	11	12	13	14	12	16	11	18	19	20	21	22	23	24	į

Exophi, Exophi, Exopopi, Drosop, Drosop, Drosop, Drosop, Propio, Ovel, Bacter, Human, Human, Staphy, Staphy, Staphy, Human, Huma	Abm83741 Human dia Add49037 Human NOV
ABU07914 ABU62941 ABB67215 ABB67214 ABB59606 ABU43213 AAU4799 ABM41318 ADS2364 ADP293106 ADP29311 ADP29311 ADP29313 ADP29313 ADP29313 ADP29313 ADP39313 ADP39313 ADP39335 ADP39035	ABM83741 ADD49037
0 0 4 4 4 0 4 0 4 0 0 0 0 C U 0 0 C C	7
126 246 246 3394 331 211 211 211 211 211 211 211 211 211	873 882
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88777799999999999999999999999999999999	4 9 9
00000000000000000000000000000000000000	44 45

ALIGNMENTS

AAY27328 standard; peptide; 27 AA. AAY27328; RESULT 1

05-NOV-1999 (first entry)

Human C9 protein fragment (residues 359-384).

CD59 mediated complement; human; Cd59 protein; C9 protein; mimetic; tumour therapy; complement-mediated inflammation; immune disorder; immunovasculitis; rheumatoid arthritis; scleroderma; C5b-9 complex.

Homo sapiens

WO9940115-A2

12-AUG-1999.

99WO-US002802 09-FEB-1999; 98US-00020393. 09-FEB-1998; (OKLA-) OKLAHOMA MEDICAL RES (BLOO-) BLOOD CENT RES FOUND

Sims PJ;

WPI; 1999-527301/44.

Compounds modulating CD59 mediated complement activity, for treatment of, e.g. immunovasculitis.

Example 2; Page 36; 75pp; English.

activity. It provides (i) molecules structurally mimicking human CD59 amino acid residues 42-58 (region which serves as binding site for CD59 - C9 interactions) when they are in a spatial orientation which can inhibit the formation of the human C59-5 complex. These mimetics specifically bind to amino acid residues 359-384 of human C9. (ii) molecules structurally mimicking C9 amino acids 359-384 when they are in a spatial orientation which can promote the formation of the C5b-9 complex. Compounds that mimic CD59 can be used to increase CD59 inhibition of C5b-9 complex assembly. This is especially useful in patients in need of suppression of complement-mediated inflammation, e.g. immune disorders and diseases such as immunovasculitis, rheumatoid arthritis, scleroderma. The invention relates to compounds modulating CD59 mediated complement

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Gaps

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Indels

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0; Mismatches

26; Conservative

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Compounds modulating CD59 mediated complement activity, for treatment of, e.g. immunovasculitis.
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Compounds that mimic C9 can be used to promote C5b-9 complex assembly. This is useful in patients in need of complement activation. The composition can be administered as an adjunct to tumour therapy. The present sequence represents a human C9 protein fragment
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD59 mediated complement; human; Cd59 protein; C9 protein; mimetic; tumour therapy; complement-mediated inflammation; immune disorder; immunovasculitis; rheumatoid arthritis; scleroderma; C5b-9 complex.
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                                                                                                                                                                       ch 100.0%; Score 140; DB 2; Length 27; 1 Similarity 100.0%; Pred. No. 1.3e-15; 26; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human C9 protein fragment (residues 334-415).
                                                                                                                                                                                                                                                                             1 CLGYHLDVSLAFSEISVGAEFNKDDC 26
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                                                                                                                                                                                                                                                                                                      CLGYHLDVSLAFSEISVGAEFNKDDC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY27324 standard; peptide; 82
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BLOOD CENT RES FOUND
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                                                                                                                                                                                                   Local Similarity
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                                                                                                                            Sequence 27 AA;
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                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                             Matches
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AAY27324

AAY27

AAY2
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     8888888
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Length 82;

Score 140; DB 2; Pred. No. 4.9e-15;

100.0%; 100.0%;

Best Local Similarity

1

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated polypeptide with human immune response associated protein (IRAP) activity. Further disclosed are polymucleotides encoding the polypeptides of the invention. The polypeptides, polymucleotides, composition, and methods are useful in diagnosing, treating, or preventing immune system, neurological, developmental, muscle, or cell proliferative disorders, disorders of lipid metabolism, obesity, and breast, colon, lung, ovarian, or prostate cancer. The current sequence represents a human immune response associated protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or preventing obesity, cancer, immune system, neurological, developmental, muscle, or cell proliferative disorders, or disorders of lipid metabolism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 human immune response associated protein; IRAP; immune system;
neurological; developmental; muscle; cell proliferative; disorder;
lipid metabolism; obesity; breast; colon; lung; ovarian; prostate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TW, Becha SD, Elliott VS, Swarnakar A;
Wang JT, Chien D, Murage J, Gera M, <sup>N</sup>
LL, Kable AE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                     Human immune response associated protein (IRAP), seq id 22.
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                                                                                                                                                                                                                                                                                                                                                                                                          anorectic; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 140; DB 8; ilarity 100.0%; Pred. No. 4.1e-14; Conservative 0; Mismatches 0;
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26
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1 CLGYHLDVSLAFSEISVGAEFNKDDC
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                                                                                                                                                                                           ADR20062 standard; protein; 474
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27-NOV-2002; 2002US-0429839P.
13-JAN-2003; 2003US-049946P.
07-FEB-2003; 2003US-04461B2P.
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                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Richardson TW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-450368/42.
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les 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                          Neuroprotective;
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                                                                                                                                                                                                                                                ADR20062;
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Matches
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gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

12-SEP-2003; 2003WO-US028227 12-SEP-2002; 2002US-0410259P.

WO2004023973-A2

25-MAR-2004

Homo sapiens

(INCY-) INCYTE CORP.

Human diagnostic and therapeutic pprotein SEQ ID NO:4192.

(first entry)

18-NOV-2004

ABM83943;

ABM83943 standard; protein; 522 AA.

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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A proposed from one of the 2722 sequences defined in the specification. A proposed from one of the invention may have a use in game therappy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, endocrine autoimmune/inflammatory disorder, developmental disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp infloring infloring infloring infloring infloring from minute biological samples, in detecting single nuclectide polymorphisms, as molecular weight markers, and for somatic or germline from minute biological samples, in detecting single nuclectide olymorphisms, as molecular weight markers, and for somatic or germline consent the sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Hartbshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegane AM, Panear IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Lagace RB, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen Pattury S, Shi X, Suarez CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
                                                                                                                                                                                                                                                                                                                                                                 Human diagnostic and therapeutic pprotein SEQ ID NO:4193.
                                                                                    ABM83944 standard; protein; 522 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-SEP-2003; 2003WO-US028227.
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                                                                                                                                                                                                                                                                       (first
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                                                                                                                                                                              ABM83944;
RESULT 4
                                                   ABM83944
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Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Everalte CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL,
Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kitton ES;
Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
Patury S, Shi X, Suarez CJ;

New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.

WPI; 2004-329368/30.

N-PSDB; ACN42595

Claim 27; Page; 190pp; English.

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The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp conclusions may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline polymorphisms, as molecular weight markers, and for somatic or germline invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from MIPO at www.wipo.int/pct/en/sequences/listing.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CLGYHLDVSLAFSEISVGAEFNKDDC 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 522 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Gaps

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0; Indels

0; Mismatches

Local Similarity 100. nes 26; Conservative

Best Loc Matches

Query Match

100.0%; Score 140; DB 8; Length 522; 100.0%; Pred. No. 4.7e-14;

RESULT

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AAW18310

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activity. It provides (1) molecules structurally minicking human CD59 amino acid residues 42-58 (region which serves as binding site for CD59 constructations) when they are in a spatial orientation which can inhibit the formation of the human C5b-9 complex. These minetics specifically bind to amino acid residues 359-384 of human C9. (ii) molecules cructurally minicking C9 amino acids 359-384 when they are in a spatial orientation which can promote the formation of the C5b-9 complex. Compounds that minic CD59 can be used to increase CD59 inhibition of C5b-0 complex assembly. This is especially useful in patients in need of suppression of complex assembly. The is especially useful in patients in need of suppression of compounds that minic C9 can be used to promote C5b-9 complex assembly. The first is encourabled inflammation, e.g. immune disorders and diseases such as immunovascultis, rheumatoid arthritis, scleroderma. Compounds that minic C9 can be used to promote C5b-9 complex assembly. The composition can be administered as an adjunct to tumour therapy. The present sequence represents a rabbit C9 protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Compounds modulating CD59 mediated complement activity, for treatment of, e.g. immunovasculitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      compounds modulating CD59 mediated complement
CD59 mediated complement; human; Cd59 protein; C9 protein; mimetic; tumour therapy; complement-mediated inflammation; immune disorder; immunovasculitis; rheumatoid arthritis; scleroderma; C5b-9 complex;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein encoded by Prokaryotic essential gene #28906.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 37.1%; Score 52; DB :
Local Similarity 36.7%; Pred. No. 1.8;
les 11; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 CLGFDLDLSLNIPGKSAGLSLTGQANKNNC 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CLGYHLDVSLAF----SEISVGAEFNKDDC
                                                                                                                                                                                                                                                                                                                          (OKLA-) OKLAHOMA MEDICAL RES FOUND.
(BLOO-) BLOOD CENT RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU43379 standard; protein; 278 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 10; 75pp; English.
                                                                                                                                                                                                                                          99WO-US002802
                                                                                                                                                                                                                                                                                  98US-00020393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus haemolyticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-527301/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 86 AA;
                                                                                                           Oryctolagus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200277183-A2
                                                                                                                                                     WO9940115-A2.
                                                                                                                                                                                                                                       09-FEB-1999;
                                                                                                                                                                                                                                                                                    09-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                           Sims PJ;
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Matches
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ABU43379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid residues 359-384 of human complement C9 are critical for binding CD59 to C9, resulting in inhibition of C5b-9 complex assembly. Peptides that mimic this human C9-derived peptides sequence, and antibodies raised against such peptides, can be used to modulate binding of CD59 to C9. The peptides bind to endogenous CD59 to prevent the CD59 complement-mediated activation of cells. Inhibition of CD59 is useful as an adjuvant for tumour therapy and as a contraceptive. The antibodies finhibit assembly of the C5b-9 complex, by binding to C9. This is useful complement-mediated cytolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modulating binding of CD59 to C9 complement component - uses agent mimics or binds the C9-specific motif, used to activate complement tumour therapy or to treat complement mediated inflammation.
                                                                                                                                                                         CD59; C5b9 complex; tumour; therapy; contraceptive;
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                                                                                                                                                                                                                                                                                                      356. .437
/label= CD59_binding_site
/note= "Claim 1 (amino acids 359-384)"
381. .406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     381 CLGYHLDVSLAFSEISVGABFNKDDC 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 33-35; 51pp; English
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                                                                                                                                                                                                                                                                                    Location/Qualifiers
  AAW18310 standard; protein; 560 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (OKLA-) OKLAHOMA MEDICAL RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY27325 standard; peptide; 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-US017940.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                      (first entry)
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Best Local Similarity 100.
Matches 26; Conservative
                                                                                                                                                                           Complement C9; CD59; C5 antibody; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-289058/26
                                                                                                                                 Human complement C9
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                                                                                                                                                                                                                                                                                                                                                                       Disulfide-bond
                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                        Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-NOV-1995;
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                                                                                      10-AUG-1997
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                                            AAW18310;
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AAY27325 ID AAY2 XX AAC AC AAY2 XX O5-N XX XX

RESULT 7

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Length 86; Indels

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Rabbit complement C9
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                                                                                                                             Disulfide-bond
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                                  Complement C9;
                                                                                                                                                                                                                                                      15-NOV-1995;
                                                                                                                                                          WO9717987-A1
                                                                                                                                                                                                                       08-NOV-1996;
                                                                                                                                                                                         22-MAY-1997.
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                                                                                                                                                                                                                                                                                                                  Sims PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                         the foll antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated or polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an compound, a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The autisense nucleic acids are useful for dentifying proteins or screening for homologous nucleic acids required for eligential proliferation of an organism. The acididate molecules for rational acids and dentifying proteins or screening for promoted acids are useful for dentifying proteins or screening for homologous nucleic acids required for profice and defented molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                 New antieense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence data for this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                          Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.1%; Score 52; DB 6; Length 278; 39.1%; Pred. No. 7.6; tive 6; Mismatches 8; Indels
                                                                                                                                                        Ohlsen KL,
Forsyth RA,
                                                                                                                                                        Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                 Claim 25; SEQ ID NO 71303; 1766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GYHLDVSLAFSEISVGAEFNKDD 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW18311 standard; protein; 561 AA
                                                                                                                                                        Malone C,
Carr GJ,
                           ; 2001US-00815242.
; 2001US-00948993.
; 2001US-0342923P.
; 2002US-00072851.
; 2002US-0362699P.
21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                           (ELIT-) ELITRA PHARM INC.
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                                                                                                                                                        Zamudio C,
Trawick JD,
                                                                                                                                                                                                      WPI; 2003-029926/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 9; Conserv
                                                                                                                                                                                                                    N-PSDB; ACA47249
                                                            25-OCT-2001;
08-FEB-2002;
06-MAR-2002;
                              21-MAR-2001;
06-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW18311;
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                                                                                                                                                          Wang L,
Wall D,
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1D AAW

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AC AAW

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modulating binding of CD59 to C9 complement component - uses agent mimics or binds the C9-specific motif, used to activate complement tumour therapy or to treat complement mediated inflammation.
CD59; C5b9 complex; tumour; therapy; contraceptive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.1%; Score 52; DB 36.7%; Pred. No. 18; iive 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CLGYHLDVSLAF----SEISVGAEFNKDDC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 36-38; 51pp; English
                                                                                                                                                                   Location/Qualifiers 389. .418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU21387 standard; protein; 405 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (OKLA-) OKLAHOMA MEDICAL RES FOUND
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                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-US017940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 36.7
                                    antibody; inflammation.
                                                                                                         Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burkholderia fungorum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-289058/26
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human; brain disease; mental disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                        WPI; 2003-857164/80.
N-PSDB; ADF55419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1449 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200277183-A2.
                                                                  JP2003245081-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-OCT-2002
                                                                                                    02-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABU25340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang L,
Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid concluding a promoter operably linked to the nucleic acid concluding a properties of sexpression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding colliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of required for proliferation, or that has an activitie cellular proliferation or the biological pathway in which a proliferation-required gene product or that has an activity against a biological pathway in which a proliferation-required gene product or that has an activitie of pathway in which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene compound's activity; (11) a culture comprising strains in which the extent conspound's activity; (11) a culture comprising strains in which the extent consponency of an organism. The antisense nucleic acids are useful for dentifying proteins or screening for homologous nucleic acids required conformant or proliferation of an organism. The antisense modeled acids required conformant proversers and addent modeled acids are useful for an addentifying processed or the screening for homologous nucleic acids required conformant proversers and acids are useful for an addentifying processed or the screening for manufacturing and acconfident modeled acids required for confident modeled acconfident modeled acconfident modeled acconfident mod
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                                                                                                                                                                                                                                        New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                     Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Indels
                                                                                                                                     Ohlsen KL,
Forsyth RA,
                                                                                                                                       Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                            Claim 25; SEQ ID NO 49311; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADF55468 standard; protein; 1449 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 GVSLEVQLATGNKKTGAEFNED 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYHLDVSLAFSEISVGAEFNKD 24
                                                                                                                                     Malone C,
Carr GJ,
21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-EEB-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 50.0%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human novel polypeptide #32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                    (ELIT-) ELITRA PHARM INC
                                                                                                                                     Zamudio C,
Trawick JD,
                                                                                                                                                                                        WPI; 2003-029926/02
                                                                                                                                                                                                          N-PSDB; ACA25257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 405 AA;
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                                                                                                                                       Wang L,
Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
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ID ADF5
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XX ADF5
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The invention relates to a DNA which encodes a novel polypeptide. A vector containing the DNA is useful as a reagent in estimation of standard substance. The antibody is useful for detecting the vector containing the DNA and for screening substances and compounds that interact specifically with the vector containing the DNA. The vector containing the DNA is used as a pharmaceutical, in treatment or as preventive agent with respect to disease e.g., brain diseases preferably mental disorders. The present sequence represents the amino acid sequence of a novel human polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                          New DNA derived from KG-1 cDNA library and encoded polypeptide, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein encoded by Prokaryotic essential gene #10867.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; SEQ ID NO 32; 401pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | | | | | : ::||:|| : |
868 YHLTVAAGSNNVNVGSEFEQLVC 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 YHLDVSLAFSEISVGAEFNKDDC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABU25340 standard; protein; 276 AA
                                                                                                                               (KAZU-) ZH KAZUSA DNA KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                            treating mental disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002US-00072851
2002US-0362699P
                                                            25-FEB-2002; 2002JP-00047501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-2002; 2002WO-US009107
25-FEB-2002; 2002JP-00047501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridium difficile
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18-FEB-1998;
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                             New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                            drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                               any one of
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacterial infection; Pseudomonas aeruginosa infection; antibacterial
                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                             The invention relates to an isolated nucleic acid comprising
                                                                                                                                                                                                                                                                                                                                                            35.0%; Score 49; DB 6; Length 276; 45.5%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                           9; Indels
                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 23;
3; Mismatches
                                                            Claim 25; SEQ ID NO 53264; 1766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas aeruginosa polypeptide #3882.
                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AB071707 standard; protein; 417 AA
                                                                                                                                                                                                                                                                                                                                                                                           4 YHLDVSLAFSEISVGAEFNKDD 25
                                                                                                                                                                                                                                                                                                                                                                                                           FHLICERYFSNIPLGIYFNEDD 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                           Query Match 35.0
Best Local Similarity 45.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa
       2003-029926/02
                N-PSDB; ACA29210.
                                                                                                                                                                                                                                                                                                                                            Sequence 276 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABO71707;
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                                                                                                                                                                                                                                                                useful as molecular targets for diagnostics, prophylaxis and treatment of
pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs,
                                                                                                                                                                                                                                         Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34.6%; Score 48.5; DB 7; Length 417; 35.3%; Pred. No. 47; ive 6; Mismatches 7; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
                                                                                                                      Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 LTWPLSSSVRFSETPVGAEYSMARAAAGRGRDEC 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome derived single exon protein #1462
                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 20453; 455pp; English.
                                                                                                                      Deloughery C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABO55228 standard; protein; 63 AA
                                                                      (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           segdata.uspto.gov/sequence.html
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                         98US-0094190P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-APR-2002; 2002US-00029386
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98US-0074788P
                                                                                                                      Rubenfield MJ, Nolling J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JUL-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 12; Conserva
                                                                                                                                                                      WPI; 2003-615309/58
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RANK D R.
HANZEL D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rank DR,
                                                                                                                                                                                            N-PSDB; ABD05278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 417 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2003194704-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                         27-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABO55228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Penn SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HANZ/)
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30-APR-2002.

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The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences conciding at least 8 amino acids of any of the 6888 amino acid sequences (ally defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially—adversable set of single exon nucleic acid molecule expression (comprising a plurality of single exon nucleic acid molecule compensable set of single exon nucleic acid molecule expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality, a single exon microarray for measuring human gene expression, a method of contiguous amino acids of any of the above—mentioned amino acids or ontiguous amino acids of any of the above—mentioned amino acids or probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above—mentioned amino acids or contiguous amino acids of any of the above—mentioned amino acids or contiguous amino acids of any of the above—mentionally are probes or microarrays to sequence (optionally with conservative amino acids substitutions), and a computer-readable methods of selling and/or licensing single exon probes or microarrays to the probes methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expression of a single exon probe cited above. The probes may be used as tools for surveying tissues to detect the presence of expression of a single exon microarray. The probes are used in in detecting and characterising grow alterations in the genomic locus that includes their exon, or in const
                                      New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus epidermidis; open reading frame; ORF; bacterial infection; antibacterial; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4518.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 48; DB 8; Length 63;
Pred. No. 5.7;
2; Mismatches 8; Indels
                                                                                                                                                     Claim 45; SEQ ID NO 28862; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CL---GYHLDVSLAFSEISVGAEFNKDD 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP39673 standard; protein; 304 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus epidermidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 50.0°
Matches 14; Conservative
WPI; 2004-119264/12.
                                                                                                              surveying tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 63 AA;
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7

4; Gaps

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ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site
                                                                                                                                                                                                                                  Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5; Length 304; 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 39;
4; Mismatches
                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 4518; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             276 IGLCYSILMALSRIRIGAHFTNDYC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LGYHLDVSLAFSEISVGAEFNKDDC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              completed: June 8, 2005, 10:40:13
                                                                                                                  (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h
Similarity 36.0%;
9; Conservative 4
                                                               97US-0055779P.
97US-0064964P.
                               98US-00134001
                                                                                                                                                ä
                                                                                                                                                  Bush
                                                                                                                                                                                   2002-381255/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                  Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Job time : 146.302 secs
                                                                                                                                                                                                   N-PSDB; ABN92218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 304 AA;
                                                               14-AUG-1997;
08-NOV-1997;
                               13-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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58265, A 12676, A 8, Appli

Sequence Seq Sequence

10, Appl 12, Appl 2, Appli 6, Appli 126, App 6, Appli 10, Appl

Sequence (Sequence (Sequence (

Sequence Sequence Sequence

5971, Ap 1528, Ap 9786, Ap 66034, A

Sequence 3 Sequence 5 Sequence 6

Sequence Sequence Sequence

78, Appl 57038, A 9, Appli 218729,

164486,

Sequence 3 Sequence

Sequence Sequence Sequence Sequence Sequence Sequence

14100,

Title: Perfect score:

Sequence:

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protein

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Run on:

Scoring table:

Database

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Methods to Inhibit the
Complement
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ADDRESSEE: Patrea L. Pabet
STREET: 2800 One Atlantic Center, 1201 W. Peachtree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: RIPM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/403,340
FILING DATE: 27-Mar-2003
CLASSIFICATION: 514
US-10-282-122A-50467

US-09-882-694-11

US-10-282-122A-71137

US-10-282-122A-71137

US-10-425-115-301836

US-10-425-115-301836

US-10-425-115-301836

US-10-36-603A-12

US-10-36-603A-12

US-10-36-603A-12

US-10-36-603A-12

US-10-36-603A-12

US-10-36-603A-12

US-10-36-603A-12

US-10-36-603A-12

US-10-36-603A-12

US-10-36-905-2

US-10-344-307A-12

US-10-36-498-11

US-10-437-963-1444861

US-10-437-963-144881

US-10-437-963-144881

US-10-377-07-78
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US-10-425-115-334893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION UNBER: US/09/020,393B
FILING DATE: 03-FEB-1998
ATTORNEY AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMFF 170
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18, Application US/10403340
Publication No. US20030166565A1
GENERAL INFORMATION:
APPLICANT: Sims, Peter J.
TITLE OF INVENTION: Compositions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 18
  CITY: Atlanta
STATE: GA
COUNTRY: USA
                US-10-403-340-18
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444.5
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  Sequence 14, Appl
Sequence 123986,
Sequence 15, Appl
Sequence 71303, PA
Sequence 53264, A
Sequence 53264, A
Sequence 28862, A
Sequence 2073, Ap.
Sequence 44593, A
Sequence 75066, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18, Appl
Sequence 14, Appl
Sequence 123986,
                                                                                             8, 2005, 10:44:17; Search time 125.767 Seconds (without alignments) 79.247 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                             Published Applications AA:*

| cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US07_NEW PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US07_NEW PUB.pep:*
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10: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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21: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
22: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
                                                                                                                                                                                                                                                                                      1710399
             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-403-340-18
US-10-403-340-14
US-10-403-340-15
US-10-403-340-15
US-10-282-122A-71303
US-10-282-122A-49311
US-10-29-386-28862
US-10-369-493-2073
US-10-369-4933
US-10-282-122A-44593
US-10-282-122A-44593
                                                                                                                                                                                                                                                                                   Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                        1710399 segs, 383334425 residues
                                                                                                                                                                                   CLGYHLDVSLAFSEISVGAEFNKDDC 26
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                                                                                                                                                       US-09-020-393B-14_COPY_26_51
140
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Maximum Match 100%
Listing first 45 summaries
                                                                       protein search, using sw model
                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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82
82
536
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662
662
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1000.0
137.9
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134.3
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Result

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Indels

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0; Mismatches

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26; Conservative
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  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/10403340
; Publication No. US20030166565A1
; GENERAL INFORMATION:
; APPLICANT: Sims, Peter J.
TITLE OF INVENTION: Compositions and Methods to Inhibit the
; C5b-9 Complex of Complement
                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 W. Peachtree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 140; DB 14; Length 82; Pred. No. 3.4e-14;
                                                                                                                                                                                                                                                                                 Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA

ZIP: 30309-3450

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BY PET COMPATION PATA:
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/403,340
FILING DATE: 27-Mar-2003
CIASSIFCATION 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 140; DB 14; Best Local Similarity 100.0%; Pred. No. 9.1e-15; Matches 26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/020,393B
FILING DATE: 03-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                );
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-403-340-14
                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-403-340-18
                                                                                                                                                                                                                                                                                                                                                                   1 CLGYHLDVSLAFSEISVGAEFNKDDC 26
                                                                                                                                                                                                                                                                                                                                                                                              CLGYHLDVSLAFSEISVGAEFNKDDC 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-873-8794
TELEFAX: 404-873-8795
TELEPHONE: 404-873-8794
TELEFAX: 404-873-8795
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 82 amino acids
                                                                                 LENGTH: 27 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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US-10-403-340-14
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US-10-47-963-123986

j Sequence 123986, Application US/10437963

j Publication No. US20040123343A1

j Publication No. US20040123343A1

j RENERAL INFORMATION:
 j APPLICANT: Ea Rosa, Thomas J.
 j APPLICANT: Cao, Yongwei
 j APPLICANT: Barbazuk, Brad
 j APPLICANT: Barbazuk, Brad
 j APPLICANT: Barbazuk, Brad
 j APPLICANT: Li, Ping
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21 (53221)B
 CURRENT APPLICATION NUMBER: US/10/437,963
 CURRENT FILING DATE: 2003-05-14
 NUMBER OF SEQ ID NOS: 204966
 SEQ ID NO 123986
 LENGTH: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sims, Peter J.
TITLE OF INVENTION: Compositions and Methods to Inhibit the Cib-9 Complex of Complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 W. Peachtree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 53; DB 16; Length 536;
Pred. No. 17;
7; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Clone ID: PAT_MRT4530_26769C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/020,393B
FILING DATE: 03-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, or CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/403,340
FILING DATE: 27-Mar-2003
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.9%; Score 53; 41.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||:|:|:||
445 LGHHGEVAKHFADLCKGAVFDADD 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 LGYHLDVSLAFSEISVGAEFNKDD 25
                              26 CLGYHLDVSLAFSEISVGAEFNKDDC
1 CLGYHLDVSLAFSEISVGAEFNKDDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-403-340-15; Sequence 15, Application US/10403340; Publication No. US20030166565A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 41.7
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: GA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-437-963-123986
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; ORGANISM: Staphylococcus haemolyticus US-10-282-122A-71303
LENGTH: 278
                                         TYPE: PRT
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APPLICANT: Vanamoco, Robert
APPLICANT: Forsyth, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: 60/202,0
PRIOR APPLICATION NUMBER: 60/202,0
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/203,347
PRIOR APPLICATION NUMBER: 60/203,347
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2001-12-02-09
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2001-12-02-09
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,636
PRIOR PILING DATE: 2001-12-02-09
PRIOR APPLICATION NUMBER: 60/253,636
PRIOR PILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/253,636
PRIOR APPLICATION NUMBER: 60/253,636
PRIOR PILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/253,636
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-03-04
PRIOR PILIN
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                                                                        OMRF 170
                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TYPOLOGY: linear
MOLECULE TYPE: peptide,
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Rabbit
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CLGYHLDVSLAF----SEISVGAEFNKDDC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLGFDLDLSLNIPGKSAGLSLTGQANKNNC 55
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                                     NUMBER: 31,284
                                                                    REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION
                                                                                                                                    TELEPHONE: 404-873-8794
TELEFAX: 404-873-8795
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
NAME: Pabst, Patrea L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Wall, Daniel
Trawick, John
Carr, Grant
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                              REGISTRATION
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US-10-282-122A-71303
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PLING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-110-23
PRIOR PLING DATE: 2000-110-23
PRIOR PLING DATE: 2000-110-23
PRIOR PLING DATE: 2000-110-23
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2001-12-26
PRIOR PLING DATE: 2001-12-26
PRIOR PLING DATE: 2001-12-26
PRIOR PLING DATE: 2001-12-26
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-06

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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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         Length 278;
                                                                                                Indels
Ouery Match 37.1%; Score 52; DB 15; Best Local Similarity 39.1%; Pred. No. 11; Matches 9; Conservative 6; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 49311, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                     120 GFAMSVGMÁLAEDHLAGKFNKDD 142
                                                                                                                                                                                       3 GYHLDVSLAFSEISVGAEFNKDD 25
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US-10-282-122A-49311
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Zyskind, Judith
Wall, Daniel
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Gaps
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                                                                          TYPE: PRT
ORCANISM: Homo sapiens
CORCANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.93
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.99
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.99
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.99
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.96
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.91
US-10-029-386-28862
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 28862
LENGTH: 63
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66;
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Pred. No. 8.3;
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LOCATION: (1)..(363)
OTHER INFORMATION: unsure at all Xaa locations
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34.3%; Score 48; DB
Best Local Similarity 36.4%; Pred. No. 66;
Matches 8; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CL---GYHLDVSLAFSEISVGAEFNKDD 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 CLLSSGYVLGVGLSFSFL-VGTEIKKQD 59
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Amelone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Yokind, Judith
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
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ORGANISM: Schizosaccharomyces pombe
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 LGYHLDVSLAFSEISVGAEFNK 23
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Best Local Similarity 50.0°
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US-10-282-122A-44593
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Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
FRIOR PELICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-09-06
PRIOR PELICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-09
PRIOR PLILNG DATE: 2000-10-23
PRIOR PLILNG DATE: 2000-10-23
PRIOR PLILNG DATE: 2000-11-27
PRIOR PLILNG DATE: 2000-11-27
PRIOR PLILNG DATE: 2000-11-27
PRIOR PLILNG DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PLILNG DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,636
PRIOR APPLICATION NUMBER: 60/257,636
PRIOR PLING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PLING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PLILNG DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 2001-02-16
PRIOR PLING DATE: 200
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CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
                                                 Sequence 53264, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 YHLDVSLAFSEISVGAEFNKDD 25
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                                                                                                                        APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                        Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Zyskind, Judith
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Best Local Similarity
Matches 10; Conserva
                        10-282-122A-53264
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PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2001-12-02

PRIOR PILING DATE: 2001-12-02

PRIOR PILING DATE: 2010-12-02

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR PILING DATE: 2011-02-16

PRIOR PILING DATE: 2011-02-16

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR APPLICATION NUMBER: 60/269,308
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APPLICANT: Carr, Grant
APPLICANT: Carr, Grant
APPLICANT: Porsyth, R.
APPLICANT: No. H.
APPLICANT: No. H.
APPLICANT: No. H.
APPLICANT: No. H.
FITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPRENCE: ELITRA.034A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 48; DB 15; Length 666;
Pred. No. 1.4e+02;
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CURRENT FILING DATE: 2003-02-20
PRIOR PEDILOCATION NUMBER: 06/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 66/230,335
PRIOR PILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 66/230,347
PRIOR PILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/240,578
PRIOR APPLICATION NUMBER: 60/245,578
PRIOR PAPLICATION NUMBER: 60/245,578
PRIOR PLING DATE: 2000-10-23
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                                PLICATION NUMBER: 60/230,335
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APPLICATION NUMBER: 60/269,308
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APPLICATION NUMBER: 60/257,931
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
FILING DATE: 2000-05-26
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Wall, Daniel
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Best Local Similarity 50.0
Matches 9; Conservative
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/201,078

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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Pred. No. 1.3e+02;
4; Mismatches 5; Indels
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APPLICATION WINBER: 60/206,848
FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 VSLAFSEISVGAEFNKDD 25
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
                            Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 50.0
Matches 9; Conservative
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Zyskind, Judith
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PRIOR PELING DATE: 2003-02-20

PRIOR PELING DATE: 2000-03-21

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PRIOR PELING DATE: 2000-05-26

PRIOR PELING DATE: 2000-09-06

PRIOR PELING DATE: 2000-09-06

PRIOR PELING DATE: 2000-10-23

PRIOR PELING DATE: 2000-10-23

PRIOR PELING DATE: 2000-11-22

PRIOR PELING DATE: 2000-11-22

PRIOR PELING DATE: 2001-01-22

PRIOR PELING DATE: 2001-01-22

PRIOR PELING DATE: 2001-01-22

PRIOR PELING DATE: 2001-02-09

PRIOR PELING DATE: 2001-02-16

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CURRENT APPLICATION NUMBER: 105/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                             Query Match 33.6%; Score 47; DB 17; Length 443; Best Local Similarity 52.6%; Pred. No. 1.2e+02; Matches 10; Conservative 3; Mismatches 6; Indels
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33.6%; Score 47; DB 15; Length 662;
Best Local Similarity 36.4%; Pred. No. 1.9e+02;
Matches 8; Conservative 6; Mismatches 8; Indels
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Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
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Yamamoto, Robert
Forsyth, R.
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      ; ORGANISM: Zea mays US-10-732-923-2707
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PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 50467
LENGTH: 690
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ITTLE OF INVENTION: Compositions and Methods for Fumonisin
ITTLE OF INVENTION: Compositions and Methods for Fumonisin
ITTLE OF INVENTION: Defeoxification
FILE REFERENCE: 3718/20825
CURRENT APPLICATION NUMBER: US/09/882,694
CURRENT PILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: 09/351,224
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 1263
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                                                                                                                                                                                                                                                                                                            Score 48; DB 15; Length 690;
Pred. No. 1.4e+02;
3; Mismatches 6; Indels
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OTHER INFORMATION: Xaa = Any Amino Acid
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923 CFGFHLSQSMEFLAIALG 940
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144 VGMALGEALLAAEFNRDD 161
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                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 50.0%;
Matches 9; Conservative
                                                                                                                                                                                                                 ; ORGANISM: Burkholderia mallei
US-10-282-122A-50467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Exophiala spinifera
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Gilliam, Jacob
Folkerts, Otto
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Matches 8; Conservative
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US-10-732-923-2707
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US-09-882-694-11
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Sequence 32121, A Sequence 3319, A Sequence 4856, A Sequence 3, Appli Sequence 61101, A Sequence 22, Appl Sequence 4307, Ap Sequence 29766, A Sequence 2536, A Sequence 25, A Se

US-09-540-236-2610 US-09-270-767-3319 US-09-270-767-48536 US-09-270-767-48536 US-09-270-767-61101 US-09-270-767-61101 US-09-311-3110-22 US-09-311-3110-22 US-09-107-433-4307 US-09-252-9311-3381 US-09-252-9311-3381 US-09-02-540-13092

Sequence Sequence Sequence Sequence

Sequence 4 Sequence 4 Sequence 4

US-09-347-798-12 US-08-565-655-4 US-08-946-967-4 US-08-361-611-4

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Query Match
Best Local Similarity
RESULT 1
US-08-559-492-3
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Matches
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Sequence 5, Appli
Sequence 4, Appli
Sequence 12, Appl
Sequence 20453, A
Sequence 6441, Appl
Sequence 11, Appl
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44012, A
11321, A
2222, Ap
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Sequence 20278, A
Sequence 16172, A
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88.222 Million cell updates/sec
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Sequence
                                                                                                                            June 8, 2005, 12:11:59 ; Search time 22 Seconds
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-313-2888-16

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US-09-949-016-10197

US-08-559-492-12

US-09-252-991A-20453

US-09-134-001C-4518

US-09-328-328-6441

US-09-328-328-6441

US-09-377-488A-11

US-09-677-488A-11

US-09-677-488A-11

US-09-677-688-11

US-09-270-767-4883

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US-09-248-796A-16130

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US-09-949-016-11321
US-09-710-279-2222
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                              Run on:
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0
Score 140; DB 2; Length 82;
Pred. No. 9e-16;
Mismatches 0; Indels
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100.0%; Pred. No. se
0; Mismatches
                                                                                                                                                                                                                                                         56
                                                                                                                                                                                                                                                                    21
                                                                                                                                                                                                                                                         1 CLGYHLDVSLAFSEISVGAEFNKDDC
                                                                                                                                                                                                                                                                26 CLGYHLDVSLAFSEISVGAEFNKDDC
                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                             26; Conservative
                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                 MOLECULE TYPE: peptide
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SOFTWARE: PatentIn Release #1.0, Version #1.25
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Patent No. 5843884;
GENERAL INFORMATION:
APPLICANT: Sims, Peter J.
TITLE OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           381 CLGYHLDVSLAFSEISVGAEFNKDDC 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  381 CLGYHLDVSLAFSEISVGAEFNKDDC 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CLGYHLDVSLAFSEISVGAEFNKDDC 26
                   олывя: US/08/559,492
15-NOV-1995
1: ^^
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Patent No. 6812339
                                                                                                                                                                    OMRF154
                                                         FILING DATE: 15-NOV-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF:
TELEPHONE: 4104-873-8794
TELEPHONE: 404-873-8795
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                               LENGTH: 560 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 26, Conservative
                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 560 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 26; Conservative
                   CURRENT APPLICATION DATA APPLICATION NUMBER: UK
                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-949-016-10197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/08559492;
Patent No. 5843884
GENERAL INFORMATION:
PAPLICANT: Sime, Peter J.
TITLE OF INFORMATION: C9 Complement Inhibitor
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 West Peachtree
               US-08-313-288B-16
Sequence 16, Application US/08313288B
Patent No. 5750502
Patent No. 5750502
Patent No. 5750502
TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN NUMBER OF SEQUENCES: 20
CORRESPONDERGES: COOPER & Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,288B FILING DATE: US/08/313,288B CLASSIFICATION: 435 ATTONEY WILE.
ATTONEY/AGENT INFORMATION:
NAME: White, John P. REGISTRATION NUMBER: 28,678
REPRENCE/DOCKET NUMBER: 40028-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEBRAX: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              378 CLGYHLDVSLAFSEISVGAEFNKDDC 403
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1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISH PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 557 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide
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                                                                                                                                                                                                                                                   CITY: New York
STATE: New York
COUNTRY: USA
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STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ANTI-SENSE: NO
US-08-313-288B-16
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US-08-559-492-5
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FATCHIAN NO. SELECTION AND GENER ASSOCIATED

TITLE OF INVENTION:
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100.0%; Score 140; DB 2; Length 560; 100.0%; Pred. No. 1.1e-14; Live 0; Mismatches 0; Indel8
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100.0%; Pred. No. 1.1e-14;
tive 0; Mismatches 0;
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ORGANISM: Pseudomonas aeruginosa
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 561 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-559-492-12
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36.0%;
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Best Local Similarity
Matches 12; Conserv
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Best Local Similarity
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Sequence 12, Application US/08559492

; Sequence 12, Application US/08559492

; Patent No. 5843884

; GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Sims, Peter J.

; TITLE OF INVENTION:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Patrea L. Pabst

STREET: 2800 One Atlantic Center, 1201 West Peachtree

STREET: Street

CITY: Atlanta

STREET: Street

CITY: Atlanta

COUNTRY: USA

ZIP: 30309-3450

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: ISP PC COMPACTED.
  ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 West Peachtree
STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Indels
                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/559,492
FILING DATE: 15-NOV-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Pabset, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/POCKET NUMBER: 31,284
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 37.1%; Score 52; DB 2
Best Local Similarity 36.7%; Pred. No. 0.4;
Matches 11; Conservative 8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PELICATION NUMBER: US/08/559,492
FILING DATE: 15-NOV-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REPERENCE/DOCKET NUMBER: OMRF154
TELECHONE: 404-873-8794
TELEFHONE: 404-873-8795
                                                                                                                                   ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 404-873-8795
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 86 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-559-492-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: si:
                                                                                                          COUNTRY: USA
ZIP: 30309-3450
                                                                                             Georgia
                                                                         Atlanta
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## Sequence 20453, Application US/09252991A
## SEQ ID NO 20453
## Sequence 20453, Application US/09252, 991A
## SEQ ID NOTED OF INVENTION: AERUGINOSA POR DIAGNOSTICS AND THERAPEUTICS
## TILLE OF INVENTION: AERUGINOSA POR DIAGNOSTICS AND THERAPEUTICS
## TILLE OF INVENTION: AERUGINOSA POR DIAGNOSTICS AND THERAPEUTICS
## TILLE OF INVENTION: AERUGINOSA POR DIAGNOSTICS AND THERAPEUTICS
## CURRENT FILLING DATE: 1999-02-18
## PRIOR FILING DATE: 1999-02-18
## PRIOR FILING DATE: 1998-02-18
## PRIOR FILING DATE: 1998-07-27
## PRIOR FILING DATE: 1998-02-18
## PRIOR PRIOR DATE: 1998-02-18
## PRIOR DATE: 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4518, Application US/09134001C

Radent No. 6380370
GENERAL INFORMATION:
FAPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: BFIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
FRIOR FILING DATE: 1997-11-08
FRIOR FILING DATE: 1997-11-08
FRIOR FILING DATE: 1997-08-14
NUMBER FOR SEQ ID NOS: 5674
SEQ ID NO 45.18
LENGTH: 304
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                                                                                                           Gaps
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Length 561;
                                                                                                           7; Indels
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Pred. No. 9.4;
     DB 2;
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Query Match 37.1%; Score 52; DB 2
Best Local Similarity 36.7%; Pred. No. 4.5;
Matches 11; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                             389 CLGFDLDLSLNIPGKSAGLSLTGQANKNNC 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.6%; Score 48.5; Dilarity 35.3%; Pred. No. 12; Conservative 6; Mismatches
                                                                                                                                                                                                            1 CLGYHLDVSLAF----SEISVGAEFNKDDC 26
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4518
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Gaps
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                                                           34.3%; Score 48; DB 4; Length 1263; ilarity 44.4%; Pred. No. 59; Conservative 4; Mismatches 6; Indels
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Pred. No. 59;
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APPLICANT: Gilliam, Jacob
APPLICANT: Folkerts, Otto
APPLICANT: Folkerts, Otto
APPLICANT: Crasta, Oswald R.
TITLE OF INVENTION: Compositions and Methods for Fumonisin
TITLE OF INVENTION: Detoxification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 35718/204101
CURRENT APPLICATION NUMBER: US/09/677,682B
CURRENT FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 09/351,224
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
; SEO ID NO 11
LENGTH: 1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: 157
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-677-682B-11
                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: 157
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-677-488A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/09677682B Patent No. 6534291
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               923 CFGFHLSQSMEFLAIALG 940
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ORGANISM: Exophiala spinifera
FEATURE:
FAMINE YEAL VARIANT
                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Exophiala spinifera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 44.4'
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                           Sequence 6441, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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Batent No. 6388171

GENERAL INPORMATION:

APPLICANT: Duvick, Jon

APPLICANT: Maddox, Joyce

APPLICANT: Gilliam, Jacob

APPLICANT: Folkerts, Otto

TITLE OF INVENTION: Compositions and Methods for Fumonisin

TITLE OF INVENTION: Detoxification

FILE REFERENCE: 5718-111

CURRENT APPLICATION NUMBER: US/09/351,224E

CURRENT FILING DATE: 1999-07-12

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 48; DB 3; Length 1263;
Pred. No. 59;
4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.3%; Score 48; DB 4; Length 663; 50.0%; Pred. No. 26; tive 4; Mismatches 5; Indels
12; Indels
4; Mismatches
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; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-351-224E-11
                                                         2 LGYHLDVSLAFSEISVGAEFNKDDC 26
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                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  923 CFGFHLSQSMEFLAIALG 940
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Best Local Similarity 44.4%;
Matches 8; Conservative
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ORGANISM: Exophiala spinifera
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Best Local Similarity 50.0°
Matches 9; Conservative
9; Conservative
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US-09-328-352-6441
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US-09-351-224E-11
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US-09-677-488A-11
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Sequence 33666, Application US/09270767

Sequence 33666, Application US/09270767

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 33666

LENGTH: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 48883, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster; FILE REFERENCE: File Reference: 7326-094
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                       34.3%; Score 48; DB 4; Length 1263; 44.4%; Pred. No. 59; tive 4; Mismatches 6; Indels
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; OTHER INFORMATION: Xaa is any amino acid US-09-882-6948-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-33666
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Best Local Similarity 44.4
Matches 8; Conservative
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US-09-270-767-33666
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RESULT 13
US-09-882-694B-11
                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

June Run on:

8, 2005, 11:17:55 ; Search time 38 Seconds (without alignments) 65.833 Million cell updates/sec

US-09-020-393B-14_COPY_26_51 Title:

140 1 CLGYHLDVSLAFSEISVGAEFNKDDC 26 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

5210 Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 26

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

88	Description	hypothetical prote	olfactory glycopro		ribosomal protein	malate dehydrogena		epidermal growth f	brain-associated s	collagen alpha 1(I	pyrroloquinoline q	hypothetical prote	fibrinogen B beta	in III	glutathione transf	cytochrome c551 -	lipid transfer pro	formaldehyde dehyd	maltose transport	lipid transfer pro	hypothetical prote	_	nitrophorin 4 - Rh	Fc gamma receptor	fumarate hydratase	-cell s	vy chain	lectin - spurge (E	Ca2+-transporting	natriuretic peptid
SUMMARIES	ΩI		A60889	A36399	JP0066	S07574	872501	S08301	A61392	165270	B32252	T46622	A48810	A60295	S71864	A36727	S38739	C46285	PC2134	S38738	PS0371	B61597	D56385	A47628	PA0062	B45895	PH1357	3612	A38386	JT0581
	DB	2	7	7	7	~	~	0	~	~	-	~	7	0	N	7	~	7	~	~	~	~	N	~	N	~	~	7	~	7
	Query Match Length	;	17	22	22	52	20	15	18	21	24	24	25	. 20	17	17	21	22	22	23	14	14	15	15	15	16	17	18	19	22
ď	Query Match	· N	20.0	20.0	19.3	19.3	18.9	18.6	18.6	18.6	18.6	18.6	18.6	17.9	17.1	17.1	17.1	17.1	17.1	17.1	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4
	Score	31	28	28	27	27	26.5	26	56	26	26			25	24	24	24	24	24	24	23	23	23	23	23	23	23	23	23	23
	Result No.	-1	2	3	4	ហ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

brain natriuretic	pyrrologuinoline g	cytochrome-c oxida	CDK inhibitor - mo	gamma-glutamyl tra	annexin V - rat (f	probable photosyst	buccalin - Califor	cartilage oligomer	conserved hypothet	major milk gland p	outer layer protei	hypothetical prote	pyrrologuinoline g	DNA-binding protei	glutathione transf
A35418	S58242	S77982	839360	859906	D53507	T07533	A35594	866215	D89854	A61526	S23981	F64121	S20453	S02146	817926
7	-	~	7	~	0	4	~	~	7	~	~	7	Н	~	7
22	24	24	25	56	56	56	11	15	16	20	20	21	23	56	24
16.4	16.4	16.4	16.4	16.4	16.4	16.1	15.7	15.7	15.7	15.7	15.7	15.7	15.7	15.7	15.4
		e	23	23	23	22.5	22	22	22	22	22	22	22	22	21.5
23	23	N	•••			~									7

ALIGNMENTS

RESULT 1
T25653
hypothetical protein C47C12.5 - Caenorhabditis elegans
C. Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T25653
R;Connell, M.
submitted to the EMBL Data Library, August 1996
A; Description: The sequence of C. elegans cosmid C47C12.
A; Reference number: Z20062
A; Accession: T25653
A;Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A;Residues: 1-22 <con></con>
A;Cross-references: EMBL:U67951; PIDN:AAB07573.1; GSPDB:GN00028; CESP:C47C12.5
A; Experimental source: strain Bristol N2; clone C47C12
C;Genetics:
B. COMO. COROD. CA1212 F.

A;Gene: CESP:C47C12.5 A;Map position: X A;Introns: 21/1

Gaps 2; 22.1%; Score 31; DB 2; Length 22; 50.0%; Pred. No. 2.9e+02; tive 2; Mismatches 5; Indels Length 22; Conservative Query Match Best Local Similarity

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4 HSDIGNSLQFSRISLKNE 21 5 HLDV--SLAFSEISVGAE 20 g ð

RESULT 2

A60889
Olfactory glycoprotein RB-8 - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: A60889
R;Schwob, J.B.; Gottlieb, D.I.
J. Neurosci. 8, 3470-3480, 1988
A;Title: Purification and characterization of an antigen that is spatially segregated in A;Reference number: A60889; MUID:89010968; PMID:3171685
A;Accession: A60889
A;Accession: A60889
A;Accession: A60889
A;Nolecule type: protein
A;Residues: 1-17 <SCH>
A;Nolecule type: protein
C;Comment: The monoclonal antibody RB-8 binds this integral membrane glycoprotein on the C;Comment: The monoclonal antibody RB-8 binds this integral membrane glycoprotein on the

Gaps ; Length 17; Query Match 20.0%; Score 28; DB 2; Length 17; Best Local Similarity 54.5%; Pred. No. 6.5e+02; Matches 6; Conservative 3; Mismatches 2; Indels

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8 VSLAFSEISVG 18

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A.Note: this protein was identified as biliverdin reductase, the identification is quest, R.Note: this protein was identified as biliverdin reductase, the identification is quest, R.Maines, M.D.; Polevoda, B.V.; Huang, T.J.; McCoubrey Jr., W.K.
Bur. J. Biochem. 235, 372-381, 1996
A.Fille: Human biliverdin IX-alpha reductase is a zinc-metalloprotein. Characterization of A.Reference number: S62622; MuID:96202961; PMID:8631357
A.Recession: S62623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: S08301
R;Nexo, E; Jorgensen, P.E.; Thim, L.; Roepstorff, P.
Biochim. Biophya. Acta 1037, 388-339, 1990
A;Title: Purification and characterization of a low and a high molecular weight form of a;Reference number: S08288; MUID:90181442; PMID:2310752
A;Accession: S08301
                                                                                                                                                                                                                                                                                                                                                                                                                protein kinase C inhibitor - human (fragment)
N;Alternate names: histidine triad nucleotide-binding protein
C;Species: Homo sapiens (man)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C;Accession: S72501; S62623
R;Maines, M.D.; Trakshel, G.M.
Arch. Biochem. Biophys. 300, 320-326, 1993
A;Title: Purification and characterization of human biliverdin reductase.
A;Reference number: S29736; MUID:9314333; PMID:8424666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drain-associated small cell lung cancer antigen - human (fragment)
NiAlternate names: BASCA
CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
CiDate: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Sep-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epidermal growth factor, high molecular weight - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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A;Residues: 1-20 «MAW>
C;Superfamily: protein kinase C inhibitor; histidine triad homology
C;Keywords: homodimer; protein kinase inhibitor; zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 20
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                                                                           Indels
80.0%; Pred. No. 1.4e+03; Mismatches 0;
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Pred. No. 1.3e+03;
2; Mismatches 1;
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A;Residues: 1-15 ×NEX>
A;Cross-references: UNIPROT:Q7M0D2
C;Keywords: growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 55.6%;
Matches 5; Conservative
                                                                           4; Conservative
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Best Local Similarity
                           Best Local Similarity
Matches 4; Conserv
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16 IGYHL 20
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807574
malate dehydrogenase (EC 1.1.1.37) - Phenylobacterium immobile (fragment)
C.Species: Phenylobacterium immobile
C.Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C.Accession: 807574
B.R. And T.O.; Hund, H.K.; Speth, A.R.; Lingens, F.
B.R. Romen Hoppe-Seyler 370, 763-768, 1989
A.Title: Purification and N-terminal amino-acid sequences of bacterial malate dehydrogen A; Reference number: 804956; MUID:89374824; PMID:2775496
A; Rocession: 807574
A; Molecule type: protein
A; Residues: 1.25 xROM>
A; Accession: 80757
A; Molecule type: Unit Residues (MUID:89374824; PMID:2775496
C; Reywords: oxidoreductase; tricarboxylic acid cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tibosomal protein L30 - Nocardia asteroides (fragment)

Cispecies: Nocardia asteroides

Cispecies: No-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004

Cipacession: JP0066

R;Ochi, K.

Bubmitted to JIPID, February 1994

A;Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal profession: JP0042

A;Accession: JP0066
                                                                                                                                                                                                              A.56399
C-type natriuretic peptide - frog
C-typecides: Nanidae gen. 8p. (frog)
C-typecides: Nanidae gen. 8p. (frog)
C-typecides: Nanidae gen. 8p. (frog)
C-type natriuretic peptide.
A.76 ference number. A.5 foreway, H., Minnamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 173, S-91-598, 1990
A.71tle: Isolation and sequence determination of frog C-type natriuretic peptide.
A.76 ference number. A.6399
A.76 ference number. A.76 ference number. A.76 ference A.76 ference number. A.76 ference n
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A;Residues: 1-22 <OCH>
A;Crost-coces: UNIRPOT:Q7M0Z8
C;Keywords: protein biosynthesis; ribosome
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DLKVTQIKSTIGAKANQKD 20
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Matches 5; Conservative
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6 ISLSKVELSVG 16
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Matches 7; Conserv
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NyAlternate names: pqq gene IV protein
C;Specias: Acinetobacter calcoaceticus
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 09-Jul-2004
C;Accession: B3252
R;Goosen, N.; Horsman, H.P.A.; Huinen, R.G.M.; van de Putte, P.
J. Bacteriol. 171, 447-455, 1989
A;Title: Acinetobacter calcoaceticus genes involved in biosynthesis of the coenzyme pyrr
A;Reference number: A32252; MUID:89123056; PMID:253663
A;Reference number: A32252; MUID:89123056; PMID:253663
A;Retus: not compared with conceptual translation
A;Molecule type: DNA
A;Reduces: 1-4 <GOO.
A;Retus: not compared with conceptual translation
A;Roosereferences: UNIPROT:P27532; GB:X06452; NID:938740; PID:9130796
A;Cross-references: UNIPROT:P27532; GB:X06452; NID:938642; PMID:1310505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gollagen alpha 1(I) chain - rat (fragment)

collagen alpha 1(I) chain - rat (fragment)

collagen satus morvegicus (Norway rat)

C;Species Rattus norvegicus (Norway rat)

C;Accession: 165270

C;Accession: 165270

C;Accession: 165270

Biochemistry 23, 6210-6216, 1984

A;Title: Construction of DNA sequences complementary to rat alpha-1 and alpha-2 collager

A;Reference number: 152392; MUID:85122694; PMID:6395893

A;Accession: 165270

A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q63076; GB:M12200; NID:g203191; PIDN:AAA40835.1; PID:g203199
C;Superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal homology
C;Accession: A61392
R;Umezawa, Y.; Kuge, S.; Kikyo, N.; Shirai, T.; Watanabe, J.; Fujiwara, M.; Okabe, T.
Jpn. J. Clin. Oncol. 21, 251-255, 1991
A;Title: Identity of brain-associated small cell lung cancer antigen and the CD56 (NKH-1A;Reference number: A61392; MUID:92046737; PMID:1719260
A;Accession: A61392
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F;16,20/Product: pyrroloquinoline quinone #status predicted <MAT>
F;16-20/Cross-link: pyrroloquinoline quinone (Glu, Tyr) #status predicted
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                                                                                                                                                                                                                                                                                                                      18.6%; Score 26; DB 2; Length 18; 46.2%; Pred. No. 1.4e+03; Live 3; Mismatches 4; Indels
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C;Superfamily: pyrroloquinoline quinone precursor pqqA
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VDIVPSQGEISVG 15
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Matches 5; Conservative
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Matches 6; Conserv
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A; Residues: 1-21 <RES>
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C;Accession: T46622
R;Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.
submitted to the EMBL Data Library, July 1995
A;Description: Cloning of a chitinase homolog which lacks chitin binding sites and is do
A;Reference number: Z23105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: A48810
R;Roberts, L.R.; Nichols, L.A.; Holland, L.J.
Biochemistry 32, 11627-11637, 1993
A;Title: Transcriptional regulation of the Xenopus laevis B beta fibrinogen subunit gene A;Reference number: A48810; MUID:94032285; PMID:8218230
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Insect Biochem. 20, 859-863, 1990
A;Title: Adipokinetic hormone causes formation of a low density lipophorin in the house
A;Reference number: A60295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-25 aROB>
A;Cross-references: UNIPROT:Q91589; GB:U05035; GB:S66373; NID:g450950; PIDN:AAA60463.1;
A;Note: sequence extracted from NCBI backbone (NCBIN:138880, NCBIP:138881)
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                                                                                                                                                                                                                                                                                               hypothetical protein c1 - loblolly pine
C;Species: Pinus taeda (loblolly pine)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fibrinogen B beta subunit - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
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C;Species: Acheta domesticus (house cricket)
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 09-Jul-2004
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Score 26; DB 1; Length 24;
Pred. No. 2e+03;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:U31309; NID:g974285; PID:g974287
A;Experimental source: strain s6PT2xs6PT3; 8 month seedlings
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.6%; Score 26; DB 2; 23.5%; Pred. No. 2e+03; cive 7; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Accession: T46622
A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 26; DB 2;
Pred. No. 2e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 SLAFSEISVGAEFNKDD 25
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40.0%;
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ilarity 41.7%;
Conservative
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                                                     4; Conservative
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                                                                                                            11 AFSEISVGAE 20
                                                                                                                                                               7 AFTDLRIGFE 16
Query Match
Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-24 <CHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A48810
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$571864
glutathione transferase (EC 2.5.1.18) class alpha 6a - pig (fragment)
NiAlternate names: glutathione 5-transferase class alpha 6a
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Accession: $71864
R;Rouimi, P.; Anglade, P.; Debrauwer, L.; Tulliez, J.
B;Colem. J. 317, 879-884, 1996
A;Title: Characterization of pig liver glutathione 5-transferases using HPLC-electrospra
A;Reference number: $71864; MUID:96332484; PMID:8760377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.Cross-references: UNIPROT: 07M3E7
A.Experimental source: liver; cytosolic
C.Comment. At least five species-independent classes of cytosolic glutathion transferase
mitochondrial form are known.
C.Complex: dimer
C.Function:
A.Description: catalyzes the nucleophilic conjugation of intracellular glutathione to a
A.Pathway: detoxification; xenobiotics metabolism
A.Note: increased hydrophilicity of GSH-conjugates facilitates their further metabolism
                             A;Residues: 1-20 <STR>
A;Cross-references: UNIPROT:Q7M484
C;Comment: This protein, a small, water-soluble apolipoprotein, is thought to increase ts a residual pathway for flight-related lipid transport.
C;Keywords: hemolymph; lipid transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
A36727
cytochrome c551 - Methylomonas sp. (fragment)
Cybece: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 09-Jul-2004
Cybate: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 09-Jul-2004
Cybacession: A36727
RyDisplatito, A.A.; Lipscomb, J.D.; Lidstrom, M.E.
J. Bacteriol: 172, 5360-5367, 1990
A;Title: Soluble cytochromes from the marine methanotroph Methylomonas sp. strain A4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 35.7%; Pred. No. 2.8e+03;
Matches 5; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                   17.9%; Score 25; DB 2; Length 20; 57.1%; Pred. No. 2.3e+03; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Note: increased hydrophilicity of GS:
es of damage
C;Superfamily: glutathione transferase
C;Keywords: dimer; transferase
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Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                              Best Local Similarity 57.1
Matches 4; Conservative
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A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-17 <DIS>
A;Molecule type: protein
A;Residues: 1-20 <STR>
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4 TTGADFN 10
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8, 2005, 11:27:39 Search completed: June 13 CSGFH 17

Job time : 40 secs

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GLUOX
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                                                                                                                         8, 2005, 11:09:50 ; Search time 166 Seconds (without alignments) 80.205 Million cell updates/sec
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Q41052
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Q91wk8
Q02gg9
Q82411
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Q82412
Q91c67
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Q91jd9
Q8jdy
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Q71gs6
Q71gs7
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Q9zz72
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               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                     1612378 segs, 512079187 residues
                                                                                                                                                                                                                       140
1 CLGYHLDVSLAFSEISVGAEFNKDDC 26
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                                                                                                                                                                                                      US-09-020-393B-14_COPY_26_51
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Maximum Match 100%
Listing first 45 summaries
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09TWH2
07FR84
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041052
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09TS69
09TS69
09Z410
08Z411
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09TR4
09JDR2
09JDR2
09JDR2
09JDR2
09JDR2
07JGS8
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Q8VL82
                                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Match Length DB
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Maximum DB seq length: 26
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polycelis n
                                                                           treponema d
clostridium
                                               xenopus lae
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                                                                                                         drosophila
                                                           chimpanzee
                                                                                                                                                                    plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- FUNCTION: Required for coenzyme pyrroloquinoline quinone (PQQ) biosynthesis. Probably provides the glutamate and tyrosine residues that are cross-linked and modified to form the coenzyme (By similarity).
-i- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.
-i- SIMILARITY: Belongs to the pqqA family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gluconobacter oxydans (Gluconobacter suboxydans).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pyrrologuinoline guinone (Glu-Tyr)
(Probable).
22131FCE0D70987D CRC64;
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0
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092274
0776X8
0776X8
078832
078832
092820
091587
091361
081361
061913
081915
071112
                                                                                                                                                                                                                                                                                                                                                   10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Coenzyme PQO synthesis protein A (Pyrroloquinoline quinone
biosynthesis protein A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34; DB 1; Length 26;
Pred. No. 8.2e+02;
2; Mismatches 5; Indels
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                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oxydans.";
FEMS Microbiol. Lett. 193:231-236(2000)
Q9ZZ74
Q7RDX8
PQQA ACICA
Q788<u>Y</u>7
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09R5S7
09R5S7
08T3M3
07M484
06F9J3
00F9J5
00F9J5
00F9J5
00F9J6
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MEDLINE=20564161; PubMed=11111029;
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NCBI_TaxID=442;
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                                                                                                                                                                                                                                                                                                                        STANDARD;
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   Diosynthesis
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les 7; Conserv
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Q7RR84
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                                                                                                                                                                                                                                                                       STRAIN-JCSC1978, and JCSC 1968;
Ito T., Okuma K., Xue M.X., Yuzawa H., Hiramatsu K.;
"Insights on antibiotic resistance of Staphylococcus aureus from its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Irato P., Piccinni E., James P., Ammermann D.;
"Evidence of a cadmium-thionein and the glycine cleavage system in
"Evidence agranulfera.";
J. Bukaryot. Microbiol. 42:376-378 (1995).
SEQUENCE 19 AA; 2381 MW; 4COB5E62B50A0984 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      community-acquired methicillin-resistant Staphylococcus aureus
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Stichotrichida, Oxytrichidae, Oxytricha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34; DB 2; Length 26;
Pred. No. 8.2e+02;
1; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            whole genome: genomic island SCC.",
Drug Resist. Updat. 6:41-52(2003).
EMBL, AB063173; BAB72134.1; -.
EMBL, AB063172; BAB72115.1; -.
Hypothetical protein.
SEQUENCE 26 AA; 3114 MW; B93553ACB62BBBA8 CRC64;
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Last annotation update)
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Last annotation update)
                                                                                                                                                          Staphylococcus aureus.
Bacteria, Firmicutes; Bacillales; Staphylococcus.
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                           26 AA.
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                                                                       Created)
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58.3%;
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01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2000 (TrEMBLrel. 14,
                                                                                                                 05-JUL-2004 (TrEMBLrel. 27,
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Best Local Similarity 58.3.,
7; Conservative
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                           PRELIMINARY;
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                                                                                              (TrEMBLrel.
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                                                                                                                                        Hypothetical protein.
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nes 6; Conserv
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                                                                                                                                                                                                      NCBI_TaxID=1280;
                                                                   01-MAR-2002
01-MAR-2002
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Q8VL82
ID Q8VL82
DT Q8VL82
DT Q1-MAR-
DT O1-MAR-
DE HYDOTHO
OS STADADJ
OX NCBL TA
RN [1] TRA
RN [1] TRA
RY TRAINE
RY HITAMAT
RY TENDEN
RY SEQUENC
RC STRAINE
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RY SEQUEN
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"Genome sequence and comparative analysis of the model rodent malaria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                           Pertea M.,
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Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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0
                                                                                                                                                                                                                                                                                           Plasmodium yoelii yoelii.
Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
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Pred. No. 3.1e+03;
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Last annotation update)
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Last annotation update)
                                                                                                                                                 23 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=12368865; DOI=10.1038/nature01099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           parasite Plasmodium yoelii yoelii.";
Nature 419:512-519(2002).
                                                                                                                                                                                           Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preliminary data.
, AABL01000229; EAA18932.1; -.
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01-MAR-2004 (TrEMBLrel. 26, Las
01-MAR-2004 (TrEMBLrel. 26, Las
Hypothetical protein (Fragment)
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66.7%;
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Best Local Similarity 66.70,
A; Conservative
24
                                       5 FTEDAEWVEYNKD 17
                                                                                                                                                 PRELIMINARY;
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12 FSEISVGAEFNKD
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                                                                                                                                                                                                                                                                              Name=PY00850;
                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=17XNL;
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Gaps

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Conservative

Matches

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Trypañosoma brucei.
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBL_TaxID=5691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith A.B., Esko J.D., Hajduk S.L.;
"Killing of trypanosomes by the human haptoglobin-related protein.";
Science 268:284-286(1995)
SEQUENCE 19 AA; 2055 MW; 65BD135667C94056 CRC64;
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MEDLINE=94043188; PubMed=8230487;
MEDLINE=94043188; PubMed-8230487;
Pardi D., Kaplan J.E., Coligan J.E., Folks T.M., Lal R.B.;
"Identification and characterization of an extended Tax protein in human T-cell lymphotropic virus type II subtype b isolates.";
D. Virol. 67:7663-7667(1993).
EMBL; S66926; AAP13991.1; -.
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Pred. No. 5.6e+03;
4; Mismatches 5; Indels
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Pred. No. 5.3e+03;
1; Mismatches 4; Indels
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Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
VCBI_TaxID=11909;
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                                                                                                                                                                                                                                                                                                                                              01-MXY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Haptoglobin-related protein beta subunit (Fragment).
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Last annotation update)
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MEDLINE=95232503; Pubmed=7716520;
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(TrEMBLrel. 01, L
(TrEMBLrel. 19, L
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Best Local Similarity 54.5%;
Matches 6; Conservative
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35.7%;
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Query Match
Best Local Similarity 35.70,
Conservative
Si Conservative
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                                                                                                                                                                                                                                                                                PRELIMINARY;
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01-DEC-2001
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"Variant forms of a group I intron in nuclear small-subunit rRNA genes of the marine red alga Porphyra spiralis var. amplifolia.";
Mol. Biol. Evol. 11:195-207(1994).
EMBL: L26175; AAA72417.1; -
NON TER 26
SEQUENCE 26 AA; 2821 MW; 9F53369E65A2254F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukāryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
NCBI_TaxID=31350;
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Nitrosomonadaceae, Nitrosomonas.
NCBI_TaxID=915;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
Var. amplifolia DNA sequence with partial cds. (Fragment).
                                                                                                                                                                                                      Length 24;
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Pred. No. 3.5e+03;
2; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                            1; Indels
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J. Biol. Chem. 268:14645-14654(1993).
Interpro; IPRO00345; CytC heme BS.
PROSITE; PS00190; CYTOCHRÖME C; UNKNOWN 1.
SEQUENCE 15 AA; 1687 MW; 983D4B8A13698849 CRC64;
                                                                                                                    7449585CEDB1AC4B CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                          Score 30; DB 2; L
Pred. No. 3.2e+03;
1; Mismatches 1;
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EMBL; AAAB01008960; EAA44199.1; -.
NON_TER 1 1
NON_TER 24 24
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MEDLINE=94224117; PubMed=8170361;
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MEDLINE=93315429; PubMed=8325841;
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2889 MW;
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Best Local Similarity 40.00,
Best Local 6; Conservative
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Best Local Similarity
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                                                                                                                    SEQÜENCE
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Q41052;
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                                                                                              SEQUENCE FROM N.A.

MEDLINE=96190544; PubMed=8627666;

Eiraku N., Novoa P., Monken C., Oliviera M.D., Oliviera O.D.,

Ishak R., Oliviera M.P., Laureiro P., Ishak M., Acevedo V.,

Hammershlak N., Zhu S.W., Kubo T., Hall W.W.,

"Identification and characterization of a new and distinct molecular

subtype of human T-cell lymphotropic virus type 2.";

J. Virol. 70:1481-1492(1996).

EMBL; U32871; AAB04905.1; -.
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Pred. No. 5.9e+03;
Sred. No. 5.9e+03;
Sred. S
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Human T-cell leukemia virus type II (HTLV-II).
Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
NCBI_TaxID=11909;
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Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
NCBL_TaxID=11909;
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Viruses, Retroid viruses, Retroviridae, Deltaretrovirus.
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Last annotation update)
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Pred. No. 5.9e+03;
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35.7%;
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Matches 5; Conservative
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MEDLINE=96190544; PubMed=8627666; Eiraku N., Novoa P., Monken C., Oliviera M.D., Oliviera O.D., Ishak R., Oliviera M.P., Laureiro P., Ishak M., Acevedo V., Hammershlak N., Zhu S.W., Kubo T., Hall W.W., Identification and characterization of a new and distinct molecular subcype of human T-cell lymphotropic virus type 2."; J. Virol. 70:1481-1492(1996).
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MEDLINE=96190544; PubMed=8627666;

MEDLINE=96190544; PubMed=8627666;

Estaku N., Novoa P., Monken C., Oliviera M.D., Oliviera O.D.,

Ishak N., Oliviera M.P., Laureiro P., Ishak M., Acevedo V.,

Hammershlak N., Zhu S.W., Kubo T., Hall W.W.;

Ildentification and characterization of a new and distinct molecular subtype of human T-cell lymphotropic virus type 2.";

J. Virol. 70:1481-1492[1996].

EMBL; U32885; AAB04925.1; -.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE=95364343; PubMed=7637327;
Kliffen M., de Jong P.T., Luider T.M.;
"Protein analyais of human maculae in relation to age-related
                                                                                                                                                                                                                                                                                                                               Score 28; DB 2; Length 21;
Pred. No. 5.9e+03;
4; Mismatches 5; Indels
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Pred. No. 5.9e+03;
4; Mismatches 5; Indels
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Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
                                                                                                                                                                                                                 EMBL, U32884; AAB04924.1; -.

NON TER 1 1 1 SEQUENCE 21 AA; 2383 MW; 11F39408575CF6D0 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
MO.2 kDa haptoglobin beta-chain homolog (Fragment).
Homo sapiens (Hunan).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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35.7%;
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Best Local Similarity 35.7%;
Matches 5; Conservative
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GO; GO:0005776; C:extracellular; IEA.
InterPro; IPR001710; Adrenomedullin.
Pfam; PF02039; Adrenomedullin; 1.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 24, Last annotation update)
PAMP-PROADRENOMEDULLIN N-terminal 20 peptide (Fragment).
Sus scrofa (Pig).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                      Query Match 19.3%; Score 27; DB 2; Length 15; Best Local Similarity 54.5%; Pred. No. 6.1e+03; Matches 6; Conservative 0; Mismatches 5; Indels
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Lab. Invest. 73:267-272(1995).
SEQUENCE 15 AA; 1649 MW; D7C94056162D5510 CRC64;
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20 AA; 2446 MW; 9604950BAF426114 CRC64;
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Matches 5; Conservative
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Title: Perfect score:

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Minimum DB Maximum DB

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Sequences AAY77154-Y77174 represent novel peptides capable of binding to and activating human fibroblast growth factor receptor (FGFR). The peptides of the invention have amino acid sequences that are unrelated to that of the human FGFR or to those of prior art FGFR-binding peptides. The peptides were isolated from phage display libraries via their ability to bind an FGFR probe. Peptide 13-1 (AAY77161) was used as the basis for the construction of an evolved phage display library, which led to the identification of further peptides (AAY77168-Y77174, consensus sequence AAY77153) capable of binding human FGFR. The peptides (or peptide mimetics) can be used to activate human FGFR, or can be used as competitive inhibitors to inhibit the binding of FGF to its receptor. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polypeptide useful as a receptor agonist or antagonist in treating wounds and promoting angiogenic capability, and as a model for designing small molecules with agonist or antagonist activity.
                                                                                                                                                                                                                                                                                                                                                    Fibroblast growth factor receptor; FGFR ligand, activation; phage display library; agonist; antagonist; drug screening; competitive inhibitor; angiogenic; wound healing.
                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                  FGFR-binding peptide 13-1, SEQ ID NO:23.
                                     ABB55986
AAU28555
AAU24984
                                                                   AAU24994
AAU26202
AAU15328
AAU15338
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ABB52357
ABB06591
ABG78526
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ADN32024
ADO78595
ADO78605
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                                                                                                                                                                                                                                                                         AAY77161 standard; peptide; 15 AA
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N-PSDB; AAZ87257.
WO200003245-A1.
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                                                                     8, 2005, 11:08:59 ; Search time 157 Seconds
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          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                 2105692 segs, 386760381 residues
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1 CLGYHLDVSLAFSEISVGAEFNKDDC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                          US-09-020-393B-14_COPY_26_51
                                                                                                                                                                                                                                                                         Listing first 45 summaries
                                                 OM protein - protein search, using sw model
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ADO16864
AAW35697
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ADN88443
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AAG73203
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                                                                                                                                                             Gapop 10.0 , Gapext 0.5
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The present invention describes a solid phase method for the synthesis of peptide-spacer-lipid conjugates, and targeted liposomes containing the conjugates. The method comprises: (a) synthesising an amino acid residue protected peptidyl resin, in solid phase; (b) conjugating a spacer and a lipid to the peptidyl resin; (c) cleaving the peptide-spacer-lipid resin; (d) removing at least one side chain protecting group from at least one amino acid of the peptide-spacer lipid, forming a peptide-spacer-lipid conjugate; and (e) subjecting the conjugate to: (i) no further processing; (ii) modifying a peptide portion of the conjugate to a cyclic form after conjugate to: (i) no further processing; (ii) modifying a peptide portion of the conjugate to a cyclic form after can of the lipid by linkage functional groups, the 2 linkage functional groups being the same or different. Also described: (l) a functional groups being the same or different. Also described: (l) a peptide-spacer-lipid conjugate, and (2) a targeted therapeutic liposome comparising a peptide-spacer-lipid conjugate, and optionally a therapeutic agent for treating a disease or a diagnostic agent for diagnosing a
                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phase synthesis; peptide-spacer-lipid conjugate; targeted liposome; tatic; somatostatin receptor 2 inhibitor;
invention also encompasses methods of screening drugs that mimic human FGF. The peptides are useful as FGFR agonist or antagonist therapeutic agents for treating wounds and promoting angiogenesis. The peptides are also useful as a model for designing small molecules which have FGFR
                                                                           agonist or antagonist activity. The peptides are stable and economical, and are alternatives to expensive recombinant FGF or FGF isolated from animal tissue. In addition, they have an improved therapeutic delivery
                                                                                                                                                                                                                                                            Gaps
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therapeutic liposomes
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                                                                                                                                                                                                                      Score 35; DB 3; Length 15;
Pred. No. 1.4e+02;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       somatostatin receptor expressed cancer; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Solid phase method, useful for synthesis of conjugates, for incorporation into targeted containing therapeutic or diagnostic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shih K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fibroblast growth factor peptide ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 14; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen L,
                                                                                                                                                                                                                                                                                                                                                                                                                                        ADL16019 standard; peptide; 15 AA.
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                                                                                                                                                                                                                25.0%;
50.0%;
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                                                                                                                                        effect and pharmacokinetics
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                                                                                                                                                                                                                                        Best Local Similarity 50.0
Matches 7; Conservative
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                                                                                                                                                                               Sequence 15 AA;
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This invention relates to a novel solid phase synthesis method for preparing peptide-spacer-lipid conjugates. Specifically, it refers to preparing peptide-FBG-lipid conjugates and it provides the various linkage groups (such as amide groups) required for such a conjugation. The present invention describes an automated method for producing a wide range of conjugates that is simple and minimises product loss during synthesis. Furthermore, the peptide-spacer-lipid can be incorporated into specific cells, and as such can be useful for the treatment and diagnosis of certain diseases including somatostatin receptor expressed cancer. Accordingly, these compositions exhibit cytostatic activity. This peptide sequence is a peptide ligand component of a conjugate of the invention.
                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Solid phase synthesis of peptide-spacer-lipid conjugates useful for synthesizing targeted therapeutic liposomes for treating or diagnosing a disease e.g. cancer involves conjugating a spacer and a linker to a
                                                     into targeted therapeutic liposomes containing therapeutic or diagnostic agents, e.g. for targeted treatment of a somatostatin receptor expressed cancer. The present sequence represents a fibroblast growth factor peptide ligand used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fibroblast growth factor peptide ligand 1 of a peptide-lipid conjugate.
                     and can be used as somatostatin receptor 2 inhibitors. The method is us for the synthesis of peptide-spacer-lipid conjugates for incorporation
disease. The peptide-spacer-lipid conjugates have cytostatic activity, and can be used as somatostatin receptor 2 inhibitors. The method is u
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FGF, fibroblast growth factor; solid phase synthesis; septide-spacer-lipid; peptide-PEG-lipid; liposome; liposomal drug delivery; somatostatin receptor expressed cancer;
                                                                                                                                                                                                                           ö
                                                                                                                                                                                       Length 15;
                                                                                                                                                                                                                         Indels
                                                                                                                                                                                     Score 35; DB 7; Le:
Pred. No. 1.4e+02;
2; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                             ADJ56718 standard; peptide; 15 AA.
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                                                                                                                                                                                         25.0%;
50.0%;
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                                                                                                                                                                                                                                                                13 SEISVGAEFNKDDC 26
                                                                                                                                                                                                                                                                                                   SALFVGAPFHVPDC 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tseng C,
                                                                                                                                                                                                                             7; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chang T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide-spacer-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptidyl resin.
                                                                                                                                                    Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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ADJ56718
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DB 8; Length 15;

25.0%; Score 35;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to a novel peptide sequences capable of translocating across a blological barrier. Furthermore, it refers to methods that use these peptides to facilitate penetration of a biologically active effector molecule such as a drug or other therapeutic agent across blological barriers e.g. epithelial or endothelial cells sealed by tight junctions. This peptide is derived from a bacterial toxin, an integral membrane or extracellular protein and can comprise an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anticoagulant, antibiotic, antipathogenic agent, immunomodulator, vitamin or enzyme. The effector molecule, however, can comprise for example insulin, gonadotropin, erythropoietin, granulocyte/monocyte colony stimulating factor (GM-CSF), enhephalin, dalargin, or neurotrophic factors. The penetrating peptide is useful for the treatment of various conditions including diabetes, infertility, hormone and vitamin deficiencies, neurodegenerative, cardiovascular, haematological and endocrine disorders, as well as obesity and neoplastic disease.

Accordingly, the peptides of this invention can be used in compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New penetrating peptide, useful for preparing a composition for treating or preventing e.g. endocrine disorders.
                                                                                                                                                                                                                                                                                                                                   diabetes;
                        Gaps
                                                                                                                                                                                                                                                                                                                                                infertility; hormone; vitamin deficiency; neurodegenerative; cardiovascular; haematological; endocrine disorder; obesity; neoplastic disease; neuroprotective; cardiant; antiarteriosclerotic;
                        ö
                                                                                                                                                                                                                                                                                                                                 penetrating peptide; epithelial; endothelial; tight junction;
                                                                                                                                                                                                                                                                                               Human neurokinin 1 (NK-1) receptor penetrating peptide 29.
                    5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
   Pred. No. 1.4e+02;
                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           osteopathic; cytostatic; nootropic.
                                                                                                                                                                                  ADB16907 standard; peptide; 23 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 14; 60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-FEB-2003; 2003WO-IB000968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-FEB-2002; 2002US-0355396P
50.08;
                                                         13 SEISVGAEFNKDDC 26
                                                                               SALFVGAPFHVPDC 15
                                                                                                                                                                                                                                                           (first entry)
 Best Local Similarity 50.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-697452/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003066859-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ben-Sasson SA,
                                                                                                                                                                                                                                                           20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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The present amino acid sequence is a pCBCI plasmid amyloid precursor protein (APP) beta-secretase cleavage site (AABO0611) (NL/KI) mutant. APP sequence containing this mutantion is less susceptible to beta-secretase cleavage. APP beta-secretase cleavage site is used to construct an artificially engineered chimeric cassette comprising human caspase-3 with interdanin linker replaced by swedish mutant beta-secretase cleavage site. This modified caspase-3 plays a pivoral role in Alzheimer's disease. Caspases are a family of cysteine proteases, that participate in the intiation and execution of apoptosis. The present invention relates to a method for functional cloning of genes encoding proteins or enzymes involved in proteolytic cleavage. The invention is based on the use of caspase expression cassettes comprising the coding sequence of a proteolytic cleavage site flanked by sequences encoding two caspase subunits. A fusion polypeptide comprising a first and a second caspase subunit, separated by a cleavage site not associated in nature, is useful for cloning gene encoding enzymes involved in proteolytic cleavage. An expression cassette containing fusion polypeptide is used to identify a mutant cell line deficient in an enzyme of interest and is also useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel fusion polypeptide comprising first and second caspase subunit separated by cleavage site not associated in nature with caspase subunit, useful for cloning gene encoding enzymes involved in proteolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for diagnosis and suppression of proliferation or metastases of a tumour cell characterised by overexpression of a polypeptide (e.g. Cathepsin B or urokinase, selectively expressed in the tumour cells). DNA encoding
                                                                                                                                                                 Amyloid precursor protein; APP; caspase; beta-secretase; cleavage site; cysteine protease; apoptosis; caspase expression cassette; metastasis; tumour; cathepsin B; urokinase; proliferation; gene therapy; interdomain linker; Alzheimer's disease; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Wild-type Leu substituted by Ile"
                                                                                                                                                                                                                                                                                                                                                                /note= "Wild-type Asn substituted by Lys"
                                                                                                                         pCBC1 APP beta-secretase cleavage site (NL/KI) mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fusion polypeptide is used in gene therapy
                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 29A; 116pp; English
AAE00613 standard; peptide; 19 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-OCT-1999; 99US-0160559P,
14-AUG-2000; 2000US-0225564P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-OCT-2000; 2000WO-US028941
                                                                                  02-JUL-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200129232-A2
                                                                                                                                                                                                                                                                              Unidentified
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                                       AAE00613;
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Gaps

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Score 34.5; DB 6; Length 23; Pred. No. 2.9e+02; Mismatches 2; Indels

24.6%; 60.0%;

Similarity 9; Conserva

Query Match Best Local S

Matches

Sequence 23 AA;

invention.

osteopathic,

that have neuroprotective, cardiant, antiarteriosclerotic, osteope cytostatic or nootropic activities. This peptide is from the humar nuerokinin 1 (NK-1) receptor and is penetrating peptide 29 of the

8 VSLAFSEISVGAEFN Conservative

Gaps

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Indels

4

Mismatches

2;

Conservative

.9

Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression vector that expresses the inhibitor from the eukaryotic cell that survives induction. The method is useful for identifying inhibitors of a protease. This sequence represents an APP mutant peptide used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method of identifying inhibitors of a procease, comprising providing a eukaryotic cell susceptible to caspase-induced apoptosis, where the eukaryotic cell expresses a gene encoding a procease and where the protease recognises a proteolytic cleavage site, introducing a fusion polypeptide expression vector into the eukaryotic cell, where the fusion polypeptide expression vector comprises an expression cassette encoding an inducible promoter that regulates a gene encoding a fusion polypeptide where the fusion polypeptide sagne encoding a fusion polypeptide where the fusion polypeptide and a gene encoding a fusion polypeptide seguence and a amino acid sequence for a first caspase subunit, a linker sequence and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protease; caspase-induced apoptosis; proteolytic cleavage site; caspase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                susceptible to caspase-induced apoptosis and isolating the cDNA expression vector that expresses the inhibitor from the eukaryotic cell
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying inhibitors of a protease by providing a eukaryotic cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 19;
       Length 19;
                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34; DB 8; 1 Pred. No. 2.7e+02;
   Score 34; DB 4; I
Pred. No. 2.7e+02;
                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                           ADO16864 standard; peptide; 19 AA.
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16-AUG-2000; 2000US-0225664P.
18-OCT-2000; 2000US-00691317.
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50.0%;
   24.3%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                that survives induction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APP mutant peptide #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-122025/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APP; mutant; mutein.
Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (LIYY/) LI Y.
(CORD/) CORDELL B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cordell B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2004018529-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                              AD016864;
                                                                                                                                         13
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                                                                                                                                                                                                                                                                                                                                       ADOLO 86.4.

I 10 ADOLO 86.4.

XXX ADOLO 86.4.

XXX ADOLO 90.1.

XXX ADOLO 90.1.

XXX                                                                                                                                                                                                                                                                                                                RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vespid venom sensitivity e.g. to Dolichovespula maculate (white face hornet), Vespula vulgaris (yellowjacket), V. maculifrons (yellowjacket), D. arenaria (yellow hornet), Polistes ammularis (wasp), P. exclamans (wasp), V. crabo (European hornet), V. flavopilosa (yellowjacket), V. germanica (yellowjacket), V. squamosa (yellowjacket), V. vidua (yellowjacket) and P. fuscatis (paperwasp)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vespid venom antigen 5 peptide fragments - useful to treat or diagnose vespid venom sensitivity.
                                                                                                                                                                                                                                    Immunomodulatory peptide; vespid antigen 5; immunogenic; allergy;
vespid venom; white face hornet wasp; immunodominant peptide; T cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bipla peptide tested for ability to block GD domain interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.3%; Score 34; DB 2; Length 20; 71.4%; Pred. No. 2.9e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                        D. maculata antigen 5 peptide (residues 91-110).
                                                                                                          AAW35697 standard, peptide, 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU77896 standard; peptide; 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fig 2; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                  97WO-US003753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
13 SEISVGAEFNKD 24
                            7 SEVKIDAEFRHD 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UYRQ ) UNIV ROCKEFELLER
                                                                                                                                                                                                                                                                                      Dolichovespula maculata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-470817/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 EFNKDDC 26
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                  11-MAR-1997;
                                                                                                                                                                                                                                                                                                                                     WO9733910-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                  11-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUN-2002
                                                                                                                                                                       13-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                    18-SEP-1997,
                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                           AAW35697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU77896;
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                                                                             RESULT 7
                                                                                            AAW35697
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97US-00908597.
                           10-APR-2001; 2001US-00828870
                                                   95US-00440391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.3%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Aib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
                                                                                                                                Lutz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conformation change.
                                                                                                                                                        WPI; 2004-247780/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:| :|||
11 CIGDEMDVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CLGYHLDVSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 AA;
                                                                                                                               Chittenden TD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
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                                                   12-MAY-1995;
                                                                  08-AUG-1997;
                                                                             25-JAN-1999;
 18-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW82186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
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                                                                                                                                                                                                                                                                                                                                                 The present invention relates to novel peptides, designated GD domains, which are capable of modulating apoptosis. The GD domains are essential for Bak's cell killing function. The GD domains mediate key protein/protein interactions with multiple cell death regulatory molecules. Also described are methods of identifying agonists or antegonists of GD domains. The methods are useful for identifying agents capable of modulating GD domain mediated heterodimerisation or homodimerisation. The methods are particularly useful in drug screening and design, e.g. for identifying agents for treating autoimmune disease or cancer, or for identifying modulators of apoptosis. The present sequence represents a peptide tested for it's ability to block GD domain-mediated interactions
                                                                                                                                                                                                                                                                       Identifying agents (e.g. modulators of apoptosis) capable of modulating GD domain mediated heterodimerization or homodimerization comprises carrying out a heterodimerization or homodimerization assay.
             GD domain, apoptosis, interaction with Bcl-XL, cell killing function,
bak; cell death regulatory molecule, autoimmune disease, cancer, bipla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anti-HIV; dermatological; immunosuppressive; antiinflammatory; antirheumatic; antiarthritic; OD domain peptide; apoptosis; protein domain; GD domain; bcl-2 related gene; Bak; cell death; immunocrossreactive protein; degenerative disorder; cell proliferation disorder; cell death disorder; asystemic lupus erythematosus; SLB; rheumatoid arthritis; acquired immunodeficiency syndrome; AIDS; Bip-1a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.3%; Score 34; DB 5; Length 20; 60.0%; Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BCl-2 related gene Bip-la GD domain peptide segid 41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADK14728 standard; peptide; 20 AA.
                                                                                                                                                                                            (APOP-) APOPTOSIS TECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                           Disclosure; Col 6; 37pp; English
                                                                                                                                                      95US-00440391.
97US-00908597.
                                                                                                                             99US-00236385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                     Lutz RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 CIGDEMDVSL 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CLGYHLDVSL 10
                                                                                                                                                                                                                                               WPI; 2002-234950/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2004054129-A1
                                                                                                                                                                                                                     Chittenden TD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20 AA;
                                                  Unidentified
                                                                           US6221615-B1
                                                                                                                             25-JAN-1999;
                                                                                                                                                      12-MAY-1995;
08-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JUN-2004
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                                                                                                     24-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADK14728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADK14728
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The invention describes an isolated and purified peptide (I) comprising unrecognised protein domain (GD domain) isolated from the bcl-2 related gene Bak that can induce cell death. (I) is useful for identifying an agent Capable of modulating GD domain radiated heterodimerisation or homodimerisation. (IV) is useful for screening a cDNA expression library for clones comprising DNA inserts encoding immunocrossreactive proteins (Claimed). An anti-(I)-antibody, its mimetics, fragments, functional equivalents and/or hybrids or its mimetics, fragments, functional equivalents and/or hybrids or its mintants, and a vector comprising a polymucleotide encoding (I) are useful as agents for treating a polymucleotide encoding (I) are useful as agents for treating proliferation or inappropriate cell death. The agents are also useful for treating disorders in which a cell is present and/or persists in an impropriate (SLE) and nheumatoid arthritis. The degenerative disorders in which a call is present and/or persists in an expremance (SLE) and nheumatoid arthritis. The degenerative disorder include acquired immunodeficiency syndrome (ALDS). This is the amino acid sequence of a Bcl-2 family member Bip-la GD domain peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "epsilon-aminocaproic acid, labelled as amino acid in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protease activity; fluorphore; detection; fluorogenic; cellular uptake;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "alpha-aminoisobutyric acid, labelled as amino acid B in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                            Novel isolated and purified peptide comprising GD domain, useful for treating degenerative disease e.g., rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fluorogenic protease indicator Swedish KM/NL AMLOID peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34; DB 8; Length 20;
Pred. No. 2.9e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 41; 38pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW82186 standard; peptide; 21 AA.
(APOP-) APOPTOSIS TECHNOLOGY INC.
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The present invention describes fluorogenic compositions which can be used for the detection of protease activity. This can be useful as an indicator of viral infection, cancer metestasis, haemophilia, emphysema, thrombosis and arthritis. The fluorogenic compositions comprise a peptide, a peptide spacer and a donor and an acceptor fluorophore. The expetide is cleaved by a protease and the fluorophores can then be detected. The present sequence is one of the peptides described in the exemplification of the invention
                                                                                                                                                                                                    New fluorogenic compositions whose fluorescence level increases in the presence of active proteases, useful for detecting and localizing protease activity in biological samples, particularly in frozen tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protease detection; peptide cleavage; enzyme activity; fluorogenic; viral infection; cancer metastasis; emphysema; arthritis; thrombosis; haemophilia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.3%; Score 34; DB 4; Length 21; 53.3%; Pred. No. 3.1e+02; ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Aib
/note= "2-aminoisobutyric acid"
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                                                                                                                                                                                                                                                                                                Disclosure; Page 27; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG73203 standard; peptide; 21 AA.
                 11-SEP-2000; 2000WO-US024882.
                                                      99US-00394019.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protease binding site #137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 SEISVGAEFN--KDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Packard BS;
                                                                                         (ONCO-) ONCOIMMUNIN INC.
                                                                                                                              Komoriya A, Packard BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ONCO-) ONCOIMMUNIN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-389573/41.
                                                                                                                                                               WPI; 2001-389573/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200118238-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
Modified-site
                                                      10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAR-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG73203;
                                                                                                                                                                                                                                                               samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                                                                                                                                                                                                        AAW82023-W82240 are peptides used in the construction of a fluorogenic composition which is used for the detection of protease activity in biological samples. The products can be used for the detection of conformation changes in nucleic acids, oligosaccharides, proteins, peptides, lipids, phopholipids, glycolipids, glycoproteins, steroids or polymers. In addition, attachment of a hydrophobic group to amolecule can be used to enhance uptake by cells. The composition is composed of P = peptide compraising a protease binding site for the protease, Fl, F2 peptides = fluorophores where Fl is attached to the amino terminal amino acid and Sl, S2 peptides = when present, are peptide spacers where S1, when present, is attached to the amino terminal acid, and S2, when present, is attached to the amino terminal acid, and S2, when
                                                                                                                                                                                                                                                                             New fluorogenic compositions - containing 2 fluorophores separated by a peptide comprising a protease binding site, used for detecting protease activity in samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protease detection; peptide cleavage; enzyme activity; fluorogenic; viral infection; cancer metastasis; emphysema; arthritis; thrombosis; haemophilia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.3%; Score 34; DB 2; Length 21; 53.3%; Pred. No. 3.1e+02; ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "modified by fluorophore"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Aib
/note= "2-aminoisobutyric acid"
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                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 28; 90pp; English
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                                                                                         98WO-US003000
                                                                                                                              97US-00802981
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                                                                                                                                                                                                      Komoriya A, Packard BS;
                                                                                                                                                                   (ONCO-) ONCOIMMUNIN INC
                                                                                                                                                                                                                                           WPI; 1998-467579/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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Modified-site
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                                                                                                                              20-FEB-1997;
                 WO9837226-A1
                                                                                         20-FEB-1998;
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                                                      27-AUG-1998
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Matches
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                                                                                                                                            used for the detection of protease activity. This can be useful as an indicator of viral infection, cancer metastasis, haemophilia, emphysema, thrombosis and arthritis. The fluorogenic compositions comprise a peptide, a peptide spacer and a donor and an acceptor fluorophore. The epptide is cleaved by a protease and the fluorophores can then be detected. The present sequence is one of the peptides described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fluorogenic composition useful for detecting protease activity and test
New fluorogenic compositions whose fluorescence level increases in the presence of active proteases, useful for detecting and localizing protease activity in biological samples, particularly in frozen tissue
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                           present invention describes fluorogenic compositions which can
                                                                                                                                                                                                                                                                                                                                                               5,
                                                                                                                                                                                                                                                                                                                           Score 34; DB 4; Length 21;
Pred. No. 3.1e+02;
                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fluorogenic; protease detection; protease inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fluorogenic protease indicator peptide #215.
                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 24; SEQ ID NO 215; 114pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             substance modulating protease activity.
                                                                                       Disclosure; Page 27; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADN88519 standard; peptide; 21 AA
                                                                                                                                                                                                                                                                                                                           24.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-JUN-2001; 2001US-00874350
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10-SEP-1999; 99US-00394019,
11-SEP-2000; 2000WO-US024882.
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SEVNLDAEFGCPKDD 20
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                                                                                                                                                                                                                                                                                                                                            Local Similarity 53.3
les 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ONCO-) ONCOIMMUNIN INC.
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                                                                                                                                                                                                                                                                                          Sequence 21 AA;
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ADN88519
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The invention relates to a fluorogenic composition (I) for detecting the activity of a protease. (I) is useful for detecting the activity of a protease. (I) is useful for detecting the activity of a crivity of protease is detected in a histological section, cell culture or tissue section. The cell suspension is derived from the biological sample chosen from tissue, blood, urine, saliva, lymph or biopsy. The protease activity is detected by fluorescence microsopy, fluorescence microplate reader, absorption microplate reader, flow cytometry, fluorometry, absorption spectroscopy or confocal fluorescent microplate reader. (I) is useful for delivering a molecule into a cell, and for screening a test agent for the ability to modulate the activity of the protease. (I) is useful for detection and localisation of protease activity in biological samples. (I) also acts as a protease inhibitor, thus useful as protease inhibitors. (I) enables detection of the protease activity, and provides a high intensity fluorescent signal at a visible wavelength when they are digested by a protease. The present sequence represents a fluorogenic protease indicator peptide of the invention.
screening a test agent for the ability to modulate the activity of the protease. (I) is useful for detection and localisation of protease activity in biological samples. (I) also acts as a protease inhibitor, thus useful as protease inhibitors. (I) enables detection of the protease activity, and provides a high intensity fluorescent signal at a visible wavelength when they are digested by a protease. The present sequence represents a fluorogenic protease indicator peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fluorogenic composition useful for detecting protease activity and test
                                                                                                                                                                                                                                             ~
                                                                                                                                                                                                  24.3%; Score 34; DB 8; Length 21; 53.3%; Pred. No. 3.1e+02; ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fluorogenic; protease detection; protease inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fluorogenic protease indicator peptide #139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 139; 114pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                substance modulating protease activity.
                                                                                                                                                                                                                                                                                                                                                                                                                         ADN88443 standard; peptide; 21 AA.
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2000WO-US024882.
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                                                                                                                                                                                                                                                                                13 SEISVGAEFN--KDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ONCO-) ONCOIMMUNIN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-399235/37.
                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2004096926-A1.
                                                                                                                                                                 Sequence 21 AA;
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10-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polynucleotide encoding a BBC3 protein which is useful for modulating apoptosis, especially in the treatment of cancer and autoimmune diseases.
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                           24.3%; Score 34; DB 8; Length 21; 53.3%; Pred. No. 3.1e+02; ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 24.3%; Score 34; DB 3; Length 26; Best Local Similarity 60.0%; Pred. No. 4e+02; Matches 6; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                             Mammalian Bik Bcl-2 homology domain 3 domain.
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                                                                                                                                                                                         AAY96324 standard; peptide; 26
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                                                                                                      6 SEVNLDAEFGXPKDD 20
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                                                          8; Conservative
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                           Query Match
Best Local Similarity
Matches 8; Conserv
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Sequence 21 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        28-OCT-1999;
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AAY96324
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Search completed: June 8, 2005, 11:24:05 Job time : 160 secs

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66.445 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/NCT_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/NCT_REW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/NCT_REW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/NSO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/NSO6_NEW_PUB.pep:*
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8: /cgn2_6/ptodata/2/pubpaa/NSO8_NEW_PUB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/NSO8_NEW_PUB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/NSO8_NEW_PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/NSO8_NEW_PUB.pep:*
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16: /cgn2_6/ptodata/2/pubpaa/NSO8_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1710399 seqs, 383334425 residues
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1 CLGYHLDVSLAFSEISVGAEFNKDDC 26
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 26
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description		Sequence 13, Appl	uence 13, Appl	uence 12, Appl	uence 13, Appl	uence 41, Appl	uence 172, App	uence 173, App	uence 139, App	uence 215, App	uence 1054, Ap	ence 1, Appli
		Desci												
SUMMARIES		ID		US-10-016-569A-13	US-10-308-644-13	US-10-816-698-12	US-10-816-698-13	US-09-828-870-41	US-09-747-287-172	US-09-747-287-173	US-09-874-350A-139	US-09-874-350A-215	US-10-083-357-1054	US-09-896-874-1
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RESULT 2

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12 9 US-09-896-139-1	ъ Б	9	15	σ	13 9 US-09-791-378-223	σ	σ	10	13 10 US-09-791-393-116	10	11	13 11 US-09-791-377-223	13 15 US-10-264-309-350			16	13 16 US-10-801-509-195	13 16 US-10-801-486-195	11	11	15	20 16 US-10-343-389A-14	σ	6	21 10 US-09-747-287-174	10 US-	11 US-	7	-	10 10 US-09-573-822C-510	10 10 US-09-573-822C-512	10 10 US-09-573-822C-514	12 9 US-09-896-874-2
12 33 23.6	13 33 23.6	14 33 23.6	15 33 23.6	16 33 23.6	17 33 23.6	18 33 23.6	19 33 23.6	~	21 33 23.6	22 33 23.6	23 33 23.6	24 33 23.6	25 33 23.6,	~	~	28 33 23.6	29 33 23.6	30 33 23.6	7	7	33 33 23.6	34 33 23.6	35 33 23.6	~	~	33 2	N	40 33 23.6	N	42 32 22.9	43 32 22.9	44 32 22.9	45 32 22.9

ALIGNMENTS

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publication US/10016569A

Sequence 13, Application US/10016569A

Publication No. US2003229013A1

GENERAL INFORMATION:
APPLICANT: Wu. Shih. Kea-Shyang

APPLICANT: Chang, Ting-Gaug

APPLICANT: Chang, Ting-Gaug

APPLICANT: Chang, Ting-Gaug

TITLE OF INVENTION: Conjugates Synthesized Thereby and Targeted Liposomes Containing

TITLE OF INVENTION: Lhe Same
TITLE OF INVENTION: Lhe Same

TITLE OF INVENTION: Lhe Same

FILE REFERENCE: P1379

CURRENT FILING DATE: 2001-12-07

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PatentIn version 3.2

SOFTWARE: PatentIn version 3.2

SOFTWARE: PatentIn version 3.2

SOFTWARE: SAME Human Cell

GOUETY MATCH

BOST Local Similarity 50.0%; Pred: No. 1.7e+02;

Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Do 2 SALEVGARFHYDDC 15
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: Peptide US-10-816-698-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Publication No. US20040054129A1
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
LUTZ. Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATE: US/09/828,870

FILING DATE: 10-Apr-2001

CLASSIFICATION: cUnknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
TITLE OF INVENTION: ANTITUMOR EFFECT OF MUTANT BIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB 17;
Pred. No. 3.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                      FILE REFERENCE: UTSC:791US
CURRENT APPLICATION NUMBER: US/10/816,698
CURRENT FILING DATE: 2004-04-02
FRIOR APPLICATION NUMBER: 60,459,901
PRIOR FILING DATE: 2003-04-02
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/236,385
FILING DATE: 25-JANURAY-1999
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 41
US-09-828-870-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
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LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.3%;
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7 CIGDEMDVSL 16
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Best Local Similarity
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      Sequence 13, Application US/10308644

Publication No. US20030229017A1

GENERAL INFORMATION:

APPLICANT: Wu, Shih-Kwang

APPLICANT: Chang, Ting-Gung

APPLICANT: Change

TITLE OF INVENTION: Conjugates Synthesized Thereby and Targeted Liposomes Containing

FILE REFERENCE: P1379

CURRENT APPLICATION NUMBER: US/10/308,644

CURRENT PILING DATE: 2002-12-03

NUMBER OF SEQ ID NOS: 29

SOFTWARE: Patentin version 3.1

FENCINCE: APPLICANT: The Change of the Conjugates of the Change of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12.
Sequence 12.
Publication No. US20050118154A1
GENERAL INFORMATION:
APPLICANT: HUNG, MIEN-CHIE
APPLICANT: LI, YAN
TITLE OF INVENTION:
CURRENT APPLICATION ANTITUMOR EFFECT OF MUTANT BIK
FILE REFERENCE: UTSC:791US
CURRENT APPLICATION NUMBER: US/10/816,698
CURRENT APPLICATION NUMBER: 2004-0.2
PRIOR APPLICATION NUMBER: 60459,901
PRIOR FILING DATE: 2003-04-02
NUMBER: OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 12.
LENGTH: 18
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APPLICANT: HUNG, MEN-CHIE
APPLICANT: LI, YAN
APPLICANT: WEN, YONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Human Cell
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Best Local Similarity
Matches 6; Conserv
US-10-308-644-13
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US-10-816-698-12
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US-09-874-350A-139

US-09-874-350A-139

Sequence 139, Application US/09874350A

Publication No. US20040096926A1

GENERAL INFORMATION:

APPLICANT: OROCIMUMIN, Inc.

APPLICANT: Monoriwanin, Inc.

APPLICANT: Remoriya, Akira

APPLICANT: Packard, Beverly

FILE REFERENCE: 300-90344015

FRIOR APPLICATION NUMBER: PCT/US98/00300

FRIOR APPLICATION NUMBER: US 09/394,019

FRIOR APPLICATION NUMBER: US 09/394,019

FRIOR APPLICATION NUMBER: US 08/802,981

FRIOR APPLICANT: PERFORMANCE: PROFILE PERFORMANCE: PROFILE PERFORMANCE: PROFILE PERFORMANCE: PROFILE PERFORMANCE: PROFILE PERFORMANCE: PE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 21;
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                                                                                                                           FEATURE:
NAME/KEY: misc_feature
LOCATION: (4)...(4)
COLER INFORMATION: Xaa is episilon-aminocaproic acid
FEATURE:
NAME/KEY: misc_feature
LOCATION: (16)...(16)
COTHER INFORMATION: Xaa is episilon-aminocaproic acid
COTHER INFORMATION: Xaa is episilon-aminocaproic acid
US-09-747-287-173
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OCATION: (3)...(3)

OTHER INFORMATION: X is Aib

NAME/KEY: MOD_RES

LOCATION: (16)...(16)

NAME/KEY: MOD_RES

LOCATION: (10)...(1)

OTHER INFORMATION: X is episilon-aminocaproic acid

NAME/KEY: MOD_RES

LOCATION: (1)...(1)

OTHER INFORMATION: K is blocked with Fmoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 24.3%; Score 34; DB 10; L
Best Local Similarity 53.3%; Pred. No. 3.7e+02;
Matches 8; Conservative 3; Mismatches 2;
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LOCATION: (4) ...(4)

COTHER INFORMATION: X is epsilon aminocaproic acid

US-09-874-350A-139
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                                               FEATURE: OTHER INFORMATION: Synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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    ORGANISM: Artificial
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; Sequence 173, Application US/09747287
; Publication No. US20030207264A1
; GENERAL INFORMATION:
; APPLICANT: ROMORIATA, AKIRA
; APPLICANT: PACKARD, BEVERLY S,
; TITLE OF INVENTION: HOWO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; TITLE OF INVENTION: HOWO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
; TITLE OF INVENTION: HOWO-DOUBLY INSTANCES INSTANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ROWORIYA, AKIRA
APPLICANT: PACKARD, BEVERLY S.
TITLE OF INVENTION: HONO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
TITLE OF INVENTION: HONO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
TITLE OF INVENTION: ACTIVITY IN BIOLOGICAL SAMPLES
FILE REFERENCE: 300-948600US
CURRENT APPLICATION NUMBER: US/09/747,287
CURRENT FILING DATE: 1090-10-10
PRIOR APPLICATION NUMBER: US/08/802,981
PRIOR FILING DATE: 1997-02-20
PRIOR APPLICATION NUMBER: PCT/US00/24882
PRIOR FILING DATE: 1997-02-20
PRIOR APPLICATION NUMBER: PCT/US00/24882
SOFTWARE: PALENT ONS: 242
SOFTWARE: PALENT NOS: 242
SOFTWARE: PALENT NOS: 242
SOFTWARE: PALENT NOS: 243
SEQ. ID NOS: 243
SEQ. ID NO 172
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Pred. No. 3.7e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (4). (4). (4)
OTHER INFORMATION: Xaa is episilon-aminocaproic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: misc_feature
; LOCATION: (16)..(16)
; OTHER INFORMATION: Xaa is episilon-aminocaproic acid
US-09-747-287-172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Synthetic peptide
                                                                                                                                                                                                                                                                                                                     ; Sequence 172, Application US/09747287; Publication No. US20030207264A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 24.3%;
Best Local Similarity 53.3%;
Matches 8; Conservative
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1 CLGYHLDVSL 10
                                                    11 CIGDEMDVSL 20
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ORGANISM: Artificial
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US-09-747-287-172
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Sequence 1, Application US/09896874
; Sequence 1, Application US/09896874
; Patent No. US20020016320A1
; GENERAL INFORMATION:
    APPLICANT: John, Varghese
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
; TITLE OF INVENTION: COMPOUNDS
; CURRENT APPLICATION NUMBER: US/09/896,874
; CURRENT APLICATION NUMBER: US 60/215,323
; RICA APPLICATION UNMBER: US 60/215,323
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LEWOTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: JOHN, Varghese
APPLICANT: JOHN, Varghese
APPLICANT: Maillaird, Michel
APPLICANT: Maillaird, Michel
APPLICANT: Maillaird, Michel
APPLICANT: Maillaird, Michel
APPLICANT: Pulley, Shon R.
TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
FILE REPERENCE: 13615_25USU4
CURRENT FILING DATE: 2001-66-29
PRIOR PELING DATE: 2001-66-29
PRIOR APPLICATION NUMBER: US 60/252,736
PRIOR APPLICATION NUMBER: US 60/255,956
PRIOR FILING DATE: 2000-11-22
PRIOR PELING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: US 60/255,956
PRIOR FILING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: US 60/259,589
PRIOR PELING DATE: 2001-02-13
PRIOR APPLICATION NUMBER: US 60/279,779
PRIOR PELING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 1
LENGTH: 12
TYPE: PRT
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Pred. No. 2.7e+02;
3; Mismatches 2; Indels
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Patent No. US2002012825A1
GENERAL INFORMATION:
APPLICANT: Beck, James P.
APPLICANT: Frang, Lawrence Y.
APPLICANT: Freskos, John N.
APPLICANT: Gailunas, Andrea
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                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
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Best Local Similarity 54.5%;
Matches 6; Conservative
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US-09-896-139-1
RESULT 11
US-09-896-874-1
                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.3%; Score 34; DB 11; Length 21; 53.3%; Pred. No. 3.7e+02; tive 3; Mismatches 2; Indels
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Publication No. US20030054370A1

GENERAL INFORMATION:

APPLICANT: Of INVENTION: Systemic Discovery of New Genes

TITLE OF INVENTION: Systemic Discovery of New Genes

FILE REFERENCE: 032796-090

CURRENT APPLICATION NUMBER: US/10/083,357

CURRENT FILING DATE: 2002-02-27

NUMBER OF SEQ ID NOS: 1346

SEQ ID NO 1054

LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Protease indicator
NAME/KEY: misc feature
LOCATION: (4). (4)
OTHER INFORMATION: Xaa is episilon-aminocaproic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (16)...(16)
OTHER INFORMATION: Xaa is episilon-aminocaproic acid
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ORGANISM: Artificial Sequence
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Matches 8; Conservative
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Best Local Similarity
Matches 9; Conserv
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US-10-083-357-1054
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                                       US-09-874-350A-215
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LENGTH: 21
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JAPPLICANT: Beyer, Brian

APPLICANT: Hammond, Gerald S

APPLICANT: Hammond, Gerald S

APPLICANT: Strickland, Corey

APPLICANT: Strickland, Corey

APPLICANT: Weng, Wenyan

APPLICANT: Weber, Patricia C

APPLICANT: Weber, Patricia C

APPLICANT: Wong, Lili

TITIE OF INVENTION: BETA-SECRETASE CRYSTALS AND METHODS FOR PREPARING THE S. TITLE OF INVENTION NUMBER: US/10/400,273

TITLE REPERENCE: JB01531-K-US

CURRENT APPLICATION NUMBER: US/10/400,273

CURRENT APPLICATION NUMBER: G0/367,937

PRIOR PILING DATE: 2002-03-27

NUMBER OF SEQ ID NOS: 5

SEQ ID NO 3

LENGTH: 12
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                                           Score 33; DB 10; Length 12;
Pred. No. 2.7e+02;
3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: cleavage sequence US-10-400-273-3
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                                             23.6%;
54.5%;
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                                           Query Match 23.6
Best Local Similarity 54.5
Matches 6; Conservative
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1 SEVNLDAEFRK 11
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SEVNLDAEFRK 12
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APPLICANT: TenBrink, Ruth E.;
TITLE OF INVENTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE;
FILE REPERENCE: 1515.41USUJ
CURRENT APPLICATION NUMBER: US/09/895,843
CURRENT PILING DATE: 2001-06-29
PRIOR PELING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
SEQ ID NO 12
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Fang, Lawrence Y.
APPLICANT: Hom, Roy
APPLICANT: Hom, Roy
APPLICANT: John, Varghese
APPLICANT: John, Varghese
APPLICANT: Maillaird, Michel
TITLE OF INVERTION: COMPOUNDS TO TREAT ALZHEIMER'S DISEASE
FILE REFERENCE: 13615.21USU1
CURRENT APPLICATION NUMBER: US 40/895,871
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,323
PRIOR APPLICATION NUMBER: US 60/215,323
PRIOR APPLICATION NUMBER: US 60/215,323
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LEWGTH: 12
                     Score 33; DB 9; Length 12;
Pred. No. 2.7e+02;
3; Mismatches 2; Indels
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Best Local Similarity 54.5%; Pred. No. 2.7e+02;
Matches 6; Conservative 3; Mismatches 2,
                                                                                                                                                                                                                                                  ; Sequence 1, Application US/09895843; Patent No. US20020143177A1; GENERAL INFORMATION:
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Jagodizinska, Barbara
John, Varghese
Maillaird, Michel
                       23.6%;
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
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                                                                                                                                                                                                                                                                                                                                    Fang, Lawrence Y.
Freskos, John N.
Gailunas, Andrea
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Query Match
Best Local Similarity 54.5%,
6; Conservative
                                                                                                       13 SEISVGAEFNK 23
                                                                                                                                 APPLICANT: Beck, James P. APPLICANT: Fang, Lawrence
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US-09-895-871-1
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117, Appl
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119, App
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                                                                                                                                                                                8, 2005, 11:18:50 ; Search time 41 Seconds (without alignments) 47.338 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                           GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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PCT-US94-01234-21
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1 CLGYHLDVSLAFSEISVGAEFNKDDC 26
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 26
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Sequence 39259, A Sequence 54476, A Sequence 1092, Appl Sequence 1093, Appl Sequence 1093, Appl Sequence 1095, Appl Sequence 2105, Appl Sequence 2105, Appl Sequence 3, Appl Sequence 4, Appli			
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7.000000000000000000000000000000000000	ALIGNMENTS	N.; GN.; AN.; AN.; AN.; AN.; AN.; AN.; 80	38; No.
US-09-2 US-09-2 US-09-5 US-09-5 US-09-5 US-09-5 US-09-2 US-09-2 US-09-1 US-08-09-1 US-08-09-1 US-08-09-1 US-08	ALIG	PC/TUS9407043A , Paul P.; Benz, G ntc	Score Pred.
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000000000000000000000000000000000000000		T. I UUBLE 1, Application P NERAL INPORMATION: APPLICANT: Tamburini, APPLICANT: Tamburini, APPLICANT: Dieter; Dr. TITLE OF INVENTION: C. TITLE OF INVENTION: C. TITLE OF INVENTION: C. TOWBURE OF SEQUENCES: COMPESSEBE: Miles In STREET: GONGCICUL COUNTRY: USA STATE: CONGCICUL COMPUTER READBLE FORM MEDIUM TYPE: Dieker COMPUTER READBLE FORM MEDIUM TYPE: Dieker COMPUTER: Sharp PC APPLICATION NUMBER: FILING DATE: May IN APPLICATION NUMBER: FILING DATE: May IN ATTORNEY/AGENT INFORMA NAME: Pamela A. Sim REGISTRATION NUMBER: FILING DATE: May INFORMA NAME: Pamela A. Sim REGISTRATION NUMBER: FILING DATE: AS SIM REGISTRATION NUMBER: TELEPROMINICATION INPORTA NAME: Pamela A. Sim REGISTRATION NUMBER: TELEPROMINICATION INPORTA NAME: Pamela A. Sim REGISTRATION NUMBER: TELEPROMINICATION INPO TELEPROMINICATION I	ı Similarity
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		14-07043A-1 nce 1, Appli RAL INFORMAT PLICANT: District D	th Sin
8		T. 1 APPLICANT: APPLICANT: APPLICANT: TITLE OF II CORRESPOND STATE: COMPUTER TELEBHON TELECHOM TEL	/ Match Local S
00000000000000000000000000000000000000		RESULT 1 Sequence 1, Application GENERAL INFORMATION: TITLE OF INVENTION: NUMBER OF SEQUENCES: CORRESPONDENCE ADDRES COUNTY: West Haven STATE: CONNECTICUT COUNTY: West Haven COUNTY: West Haven STATE: CONNECTICUT COUNTY: West Haven COU	Query Best L
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Gaps

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GENERAL INFORMATION:
APPLICANT: King, Te P.
TITLE OF INVENTION:
TITLE OF INVENTION:
ANTIGEN 5
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE:
COUNTRY: USA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB 3; Length 20;
Pred. No. 61;
1; Mismatches 1; Indels
                                                                                                                                                                                        Score 34; DB 1; Length 20;
Pred. No. 61;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/614,935
FILING DATE: 11-MAR-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 17, Application US/09130287
Patent No. 6106844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                            24.3%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 24.3%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 amino acids
20 amino acids
                TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                        Query Match
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                ANTI-SENSE: NO
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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5 DFNHDDC 11
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US-09-130-287-17
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                                                                                                                                                                                                                                                                                                                                                                                     US-09-130-287-17
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                                                                                                                              RESULT 2
US-09-351-657A-36
US-09-351-657A-36
is Sequence 36, Application US/09351657A
js Patent No. 6545140
is GENREALI INFORMATION:
APPLICANT: Harmon, Barry G.
APPLICANT: Jackwood, Mark W.
APPLICANT: Brockus, Charles W.
TITLE OF INVENTION: DNA encoding an avian beta-defensin and uses thereof;
FILE REPERBNCE: 757.007US1
CURRENT FILING DATE: 1999-07-13
FRIOR FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 26
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  4; Indels
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| Patent No. 5804201
| GENERAL INFORMATION:
| APPLICANT: King, Te P. TITLE OF INVENTION: IMMUNOMODULATORY PEPTIES OF VESPID TITLE OF INVENTION: ANTIGEN 5
| NUMBER OF SEQUENCES: 81
| CORRESPONDENCE ADDRESS: ADDRESSE: David A. Jackson, Esq.
| STREET: Floor STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/614,935
FILING DATE: 11-MAR-1996
CLASSIFICATION: 436
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35.0%; Pred. No. c.,
Mismatches
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NAME: Jackenn Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-156
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPAX: 201-343-1684
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Best Local Similarity 35.07
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2 SEVKMDAEFRHDD 14
                                      13 SEISVGAEFNKDD 25
7; Conservative
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STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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US-08-614-935-17
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  Matches
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US-08-659-984A-18

| Sequence 18, Application US/08659984A |
| Sequence 18, Application US/08659984A |
| Patent No. 5942400 |
| GENERAL INFORMATION: APPLICANT: Anderson, John P. APPLICANT: Jacobson-Croak, Kirsten L. APPLICANT: Jacobson-Croak, Kirsten L. TITLE OF INVENTION: Inhibition |
| TITLE OF INVENTION: Inhibition |
| NUMBER OF SEQUENCES: 21 |
| CORRESPONDENCE ADDRESS: ADDRESSE: Townsend and Townsend and Crew LLP |
| STREET: Two Embarcadero Ctr., 8th Floor |
| CITY: San Francisco |
| STREET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 21;
                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/802,981 FILING DATE: 20-FEB-1997 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A FILING DATE: 07-JUN-1996 CLASSIFICATION: 436
                                                                                                                                                                    NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 016865-000300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 24.3%; Score 34; DB 3; Best Local Similarity 53.3%; Pred. No. 65; Matches 8; Conservative 3; Mismatches ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 3
OTHER INFORMATION: /product= "Aib"
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OTHER INFORMATION: /product= "Acp"
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APPLICATION NUMBER: US 08/485,152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                           PC-DOS/MS-DOS
    IBM PC compatible
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6 SEVNLDAEFGXPKDD 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide FEATURE:
                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
    COMPUTER:
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Patent No. 6037137
CENERAL INFORMATION:
APPLICANT: Packard, Beverly S.
TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof NUMBER OF SEQUENCE: 231
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LiP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEY/AGENT INVOCATION NUMBER: 32,073
REGISTRATION NUMBER: (C) ATTORNEY DOCKET NO. 104322.147CIP
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Sequence 41, Application US/09236385A

Sequence 41, Application US/09236385A

GENERAL INFORMATION:

APPLICANT: CHITTENDEN, Thomas D.; and

LUTZ, Robert J.

TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH

MODULATE APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,385A
FILING DATE: 25-Jan-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.3%; Score 34; DB 3; Length 20; 60.0%; Pred. No. 61; 2; Indels tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 202-942-8400
TELEFAX: 202-942-6484
INFORMATION FOR SEQ ID NO: 41
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:| :||||
11 CIGDEMDVSL 20
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: | | | | | | | DFNHDDC 11
                                                                                        RESULT 5
US-09-236-385A-41
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US-08-802-981-112
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2; Gaps

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JESULA Application US/08802981

| Sequence 114, Application US/08802981
| Sequence 114, Application US/08802981
| Patent No. 6037137
| GENERAL INFORMATION:
| APPLICANT: Romoriya, Akira
| APPLICANT: Packard Beverly S.
| TITLE OF INVENTION: Compositions for the Detection of Enzyme
| TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
| TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
| NUMBER OF SEQUENCES: 231
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Two Embarcadero Center, Eighth Floor
| STREET: Two Embarcadero Center, Eighth Floor
| STREET: Control of Enzyme
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
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                                                                                                                                                                         Ouery Match 23.6%; Score 33; DB 3; Length 21; Best Local Similarity 53.3%; Pred. No. 96; Matches 8; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DUSS/MS-DUSS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,981
FILING DATE: 20-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HUnter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 016865-000300US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTER.STICS:
OTHER INFORMATION: /product= "Acp" FRATURE: NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 3
OTHER INFORMATION: /product= "Aib"
                                                                           ) LOCATION: 16
; OTHER INFORMATION: /product= "Acp"
US-08-802-981-113
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OTHER INFORMATION: /product= "Acp"
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US-08-802-981-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                 13 SEISVGAEFN--KDD 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNES:
TOPOLLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                               6 SEVKLDAEFGXPKDD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Modified-site LOCATION: 16
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Best Local Similarity 53.3
Matches 8; Conservative
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APPLICANT: ROMORIYA, Akira
APPLICANT: ROMORIYA, Beverly S.
TITLE OF INVENTION: Compositions for the Detection of Enzyme
TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
TORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Bighth Floor
CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 21; 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,981
FILING DATE: 20-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HUNTER: 70m
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 016865-000300US
TELEFORMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: LAND ACIDS
                    ATTORNEY/AGENT INCORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REERENCE/DOCKET NUMBER: 15270-002810US
TELEPHONE: 415-326-2400
TELEPHONE: 415-326-2422
INFORMATION FOR SEQ ID NO. SEQUENCE CHARACTERISTICS:
LENGTH: 21 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  23.6%; Score 33; 50.0%; Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 3
OTHER INFORMATION: /product= "Aib"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
US-08-802-981-113
; Sequence 113, Application US/08802981
; Patent No. 6037137
     FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Modified-site LOCATION: 4
                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 50.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 SEISVGAEFNKD 24
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MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS:
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US-08-313-200-8

Sequence B, Application US/08313200

Patent No. 5998153

GENERAL INFORMATION:

APPLICANT: Baker, James R.

APPLICANT: Roenig, Ronald J.

TITLE OF INVENTION: THYROID PEROXIDASE EPITOPIC REGIONS

NUMBER OF SEQUENCES: 13

CORRESPONDENCES: 13

CORRESPO
                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 4; Length 21; Pred. No. 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.9%; Score 32; DB 2; Length 22; 54.5%; Pred, No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,200
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.5e+02;
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NAME: Konski, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 20344-20658.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 96;
1; Mismatches
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SEQ ID NOS 8
LENGTH: 21
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                      23.6%;
ilarity 63.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 SEISVGAEFNK 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | : ||| ||
10 SRLDTGAELNK 20
                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-09-854-864-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 94304-1018
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; Patent No. 6774106
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: TU, GANG
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-666B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Pred. No. 96;
3; Mismatches 3; Indels
                                                                                                                                                                                                           Sequence 18, Application US/08660531
Sequence 18, Application US/08660531
Sequence 18, Application US/08660531
Sequence 18, Application
APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Keim, Pamela S.
APPLICANT: Keim, Pamela S.
APPLICANT: Anderson, John P.
TITLE OF INVENTION: Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heellin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002210US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.6%;
50.0%;
                                   SEISVGAEFN--KDD 25
                                                                                             SEVKMDAEFGXPKDD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 21 amino acids
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Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 SEISVGAEFNKD 24
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SEVNLDAEFRHD 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: peptide US-08-660-531-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-09-854-864-8
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TYPE: amino acid
TYPCIOGY: linear
HOLECULE TYPE: peptide
FRAGENT TYPE: internal
ORIGINAL SOURCE:
ORIGINAL SURCE:
TISSUE TYPE: Root
US-08-324-301-3
                                                                                                                                                                                                            22.1%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: No. 6368792e
US-09-049-698-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                           Query Match
Best Local Similarity 60.0.
Best Local 6; Conservative
19 amino acids
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                   7 DVSLAFSEIS 16
                                                                                                                                                                                                                                                                                                                                           2 NIELGFSEIS 11
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US-09-049-698-42
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Patent No. 5597569
GENERAL INFORMATION:
APPLICANT: Siegall, Clay B.
APPLICANT: Gavlar, Susan L.
APPLICANT: Marquardt, Hans
TITLE OF INVENTION: A NEW RIBOSOME-INACTIVATING PROTEIN
TITLE OF INVENTION: ISOLATED FROM THE PLANT BRYONICA DIOICA
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                           APPLICANT: Baker, James R.
APPLICANT: Recaig, Ronald J.
APPLICANT: Koenig, Ronald J.
APPLICANT: William Septicant J.
APPLICANT: University of Michigan
TITLE OF INVENTION: THYROID PEROXIDASE EPITOPIC REGIONS
FILE REFERENCE: 203442065801
CURRENT APPLICATION NUMBER: US/09/251,039
CURRENT PILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: 08/313,200
EARLIER APPLICATION NUMBER: 07/885,656
EARLIER PILING DATE: 1992-05-19
EARLIER PILING DATE: 1993-04-22
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 12
LENGTH: 22
LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.9%; Score 32; DB 4; Length 22; 54.5%; Pred. No. 1.5e+02; ive 1; Mismatches 4; Indels
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ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Bristol-Myers Squibb Company
STREET: 3005 First Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFTCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/141,891
FILING DATE: 25-0CT-1993
ATTORNEY/AGENT INFORMATION:
NAME: POOR, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: 32,928
TELECOMMUNICATION:
TELEPHONE: 206-728-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/324,30
             Sequence 12, Application US/09251039
Patent No. 6528059
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 206-727-3601
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 22.9
Best Local Similarity 54.5
Matches 6; Conservative
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10 SRLDTGAELNK 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-251-039-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-08-324-301-3
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REAGENTS AND METHODS FOR THE USEFUL FOR DETECTING DISEASES OF THE GASTROINTESTINAL TRACT
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                                                 Gaps
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Score 31, DB 1, Length 19;
Pred. No. 1.8e+02;
2; Mismatches 2; Indels
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SURTWARE: FastSEO for Windows Version 2.0
SURRENT APPLICATION DAY:
APPLICATION NUMBER: US/09/049,698
                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: BILLING-WEDEL, PATRICIA A.
APPLICANT: COLETY, MAURICE
APPLICANT: COLETY, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: HAYDEN, MARK
APPLICANT: HAYDEN, MARK
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS
TITLE OF INVENTION: TRACT
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS: ADDOCT LABORACCISES
CORRESPONDENCE ADDRESS: ADDOCT LABORACCISES
STREET: 100 ADDOCT PARK ROAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6068.US.P1
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                                                          0; Gaps
Query Match 22.1%; Score 31; DB 3; Length 21; Best Local Similarity 60.0%; Pred. No. 2.1e+02; Matches 6; Conservative 2; Mismatches 2; Indels
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15 ISVGAEFNKD 24 |:||:||| 8 ITVNAKMNKD 17

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Search completed: June 8, 2005, 11:28:25 Job time: 42 Becs

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